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(54) Title: HUMAN CANCER ASSOCIATED GENE SEQUENCES AND POLYPEPTIDES

(57) Abstract

This invention relates to newly identified tissue specific cancer associated polynucleotides and the polypeptides encoded by these polynucleotides herein collectively known as "cancer antigens", and to the complete gene sequences associated therewith and to the expression products thereof, as well as the use of such tissue specific cancer antigens for detection, prevention and treatment of tissue specific disorders, particularly the presence of cancer. This invention relates to the cancer antigens as well as vectors, host cells, antibodies directed to cancer antigens and recombinant and synthetic methods for producing the same. Also provided are diagnostic methods for diagnosing and treating, preventing and/or prognosing tissue specific disorders, including cancer, and therapeutic methods for treating such disorders. The invention further relates to screening methods for identifying agonists and antagonists of cancer antigens of the invention. The present invention further relates to methods and/or compositions for inhibiting the production and/or function of the polypeptides of the present invention.

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Human Cancer Associated Gene Sequences and Polypeptides

Field of the Invention

This invention relates to newly identified tissue specific cancer associated polynucleotides and the polypeptides encoded by these polynucleotides herein collectively known as "cancer antigens," and to the complete gene sequences associated therewith and to the expression products thereof, as well as the use of such cancer antigens for detection, prevention and treatment of tissue specific diseases, particularly cancers. This invention relates to the cancer antigens as well as vectors, host cells, antibodies directed to cancer antigens and recombinant and synthetic methods for producing the same. Also provided are diagnostic methods for diagnosing and treating, preventing and/or prognosing disorders related to tissue specific diseases, including cancer, and therapeutic methods for treating such disorders. The invention further relates to screening methods for identifying agonists and antagonists of cancer antigens of the invention. The present invention further relates to methods and/or compositions for inhibiting the production and/or function of the polypeptides of the present invention.

Background of the Invention

Cell growth is a carefully regulated process which responds to specific needs of the body. Occassionally, the intricate, and highly regulated controls dictating the rules for cellular division break down. When this occurs, the cell begins to grow and divide independently of its homeostatic regulation resulting in a condition commonly referred to as cancer. In fact, cancer is the second leading cause of death among Americans aged 25-44.

Cancers or malignant tumors are characterized by continuous cell proliferation and cell death. Cancer cells have been shown to exhibit unique gene expression, and dozens of cancer-specific genetic markers, tumor antigens, have been identified. P35B, a tumor rejection antigen, was first identified in mouse. A point mutation in the P35B gene elicits a cytolytic T lymphocyte response but no detectable antibody response (Szikora, J. P. et al. (1990) EMBO J. 9:1041-1050). A human homolog of P35B, FX, is a homodimeric

NADP(H)-binding protein of 68 kDa. FX acts as a combined epimerase and NADPH-dependent reductase in converting GDP-4-keto-6-D-deoxymannose to GDP-L-fucose (Tonetti, M. et al. (1996) J. Biol. Chem. 271: 27274-27279). GDP-L-fucose is the substrate of several facosyl-transferases involved in the biosysthesis of blood group ABH antigenic determinants. GDP-L-fucose is also utilized in synthesizing fucosylated glycoproteins and glycolipids which function in cell adhesion and recognition (Springer, T. A. and Lasky, L. A. (1991) Nature 329: 196-197; Brandley, B. K. et al. (1990) Cell 63: 861-863; and Feizi, T. and Childs, R. A. (1987) Biochem. J. 245: 1-11).

Thus, there is a need for the identification and characterization of novel tissue specific polynucleotides and polypeptides which modulate activation and differentiation of cells, both normally and in disease states. In particular, there is a need to isolate and characterize additional molecules that mediate apoptosis, DNA repair, tumor-mediated angiogenesis, genetic imprinting, immune responses to tumors and tumor antigens and, among other things, that can play a role in detecting, preventing, ameliorating or correcting dysfunctions or diseases.

Summary of the Invention

The present invention includes isolated nucleic acid molecules comprising, or alternatively, consisting of, a cancer associated polynucleotide sequence disclosed in the sequence listing (as SEQ ID NOs:1 to 842) and/or contained in a human cDNA clone described in Tables 1, 2 and 5 and deposited with the American Type Culture Collection ("ATCC"). Fragments, variant, and derivatives of these nucleic acid molecules are also encompassed by the invention. The present invention also includes isolated nucleic acid molecules comprising, or alternatively consisting of, a polynucleotide encoding a cancer polypeptide. The present invention further includes cancer polypeptides encoded by these polynucleotides. Further provided for are amino acid sequences comprising, or alternatively consisting of, cancer polypeptides as disclosed in the sequence listing (as SEQ ID Nos: 843 to 1684) and/or encoded by a human cDNA clone described in Tables 1, 2 and 5 and deposited with the ATCC. Antibodies that bind these polypeptides are also encompassed by the invention. Polypeptide fragments, variants, and derivatives of these amino acid sequences are also encompassed by the invention, as are polynucleotides encoding these polypeptides and antibodies that bind these polypeptides. Also provided are diagnostic methods for diagnosing

and treating, preventing, and/or prognosing disorders related to cancer, and therapeutic methods for treating such disorders. The invention further relates to screening methods for identifying agonists and antagonists of cancer antigens of the invention.

Detailed Description

Tables

Table 1 summarizes some of the cancer antigens encompassed by the invention (including contig sequences (SEQ ID NO:X) and the cDNA clone related to the contig sequence) and further summarizes certain characteristics of the cancer polynucleotides and the polypeptides encoded thereby. The first column shows the "SEQ ID NO:" for each of the 842 cancer antigen polynucleotide sequences of the invention. The second column provides a unique "Sequence/Contig ID" identification for each cancer associated sequence. The third column, "Gene Name," and the fourth column, "Overlap," provide a putative identification of the gene based on the sequence similarity of its translation product to an amino acid sequence found in a publicly accessible gene database and the database accession no. for the database sequence having similarity, respectively. The fifth and sixth columns provide the location (nucleotide position nos. within the contig), "Start" and "End", in the polynucleotide sequence "SEQ ID NO:X" that delineate the preferred ORF shown in the sequence listing as SEQ ID NO:Y. The seventh and eighth columns provide the "% Identity" (percent identity) and "% Similarity" (percent similarity), respectively, observed between the aligned sequence segments of the translation product of SEQ ID NO:X and the database sequence. The ninth column provides a unique "Clone ID" for a cDNA clone related to each contig sequence. The tenth column shows the tissue in which each SEQ ID NO:X is predominantly expressed.

Table 2 summarizes ATCC Deposits, Deposit dates, and ATCC designation numbers of deposits made with the ATCC in connection with the present application.

Table 3 indicates public ESTs, of which at least one, two, three, four, five, ten, fifteen or more of any one or more of these public EST sequences are optionally excluded from certain embodiments of the invention.

Table 4 lists residues comprising antigenic epitopes of antigenic epitope-bearing fragments present in most of the cancer associated polynucleotides described in Table 1 as predicted by the inventors using the algorithm of Jameson and Wolf, (1988) Comp. Appl.

Biosci. 4:181-186. The Jameson-Wolf antigenic analysis was performed using the computer program PROTEAN (Version 3.11 for the Power MacIntosh, DNASTAR, Inc., 1228 South Park Street Madison, WI). Cancer associated polypeptides (e.g., SEQ ID NO:Y, polypeptides encoded by SEQ ID NO:X, or polypeptides encoded by the cDNA in the referenced cDNA clone) may possess one or more antigenic epitopes comprising residues described in Table 4. It will be appreciated that depending on the analytical criteria used to predict antigenic determinants, the exact address of the determinant may vary slightly. The residues and locations shown in column two of Table 4 correspond to the amino acid sequences for most cancer associated polypeptide sequence shown in the Sequence Listing.

Table 5 shows the cDNA libraries sequenced, and ATCC designation numbers and vector information relating to these cDNA libraries.

Definitions

The following definitions are provided to facilitate understanding of certain terms used throughout this specification.

In the present invention, "isolated" refers to material removed from its original environment (e.g., the natural environment if it is naturally occurring), and thus is altered "by the hand of man" from its natural state. For example, an isolated polynucleotide could be part of a vector or a composition of matter, or could be contained within a cell, and still be "isolated" because that vector, composition of matter, or particular cell is not the original environment of the polynucleotide. The term "isolated" does not refer to genomic or cDNA libraries, whole cell total or mRNA preparations, genomic DNA preparations (including those separated by electrophoresis and transferred onto blots), sheared whole cell genomic DNA preparations or other compositions where the art demonstrates no distinguishing features of the polynucleotide/sequences of the present invention.

As used herein, a "polynucleotide" refers to a molecule having a nucleic acid sequence contained in SEQ ID NO:X (as described in column 1 of Table 1) or the related cDNA clone (as described in column 9 of Table 1 and contained within a library deposited with the ATCC). For example, the polynucleotide can contain the nucleotide sequence of the full length cDNA sequence, including the 5' and 3' untranslated sequences, the coding region, as well as fragments, epitopes, domains, and variants of the nucleic acid sequence.

Moreover, as used herein, a "polypeptide" refers to a molecule having an amino acid sequence encoded by a polynucleotide of the invention as broadly defined (obviously excluding poly-Phenylalanine or poly-Lysine peptide sequences which result from translation of a polyA tail of a sequence corresponding to a cDNA).

In the present invention, "SEQ ID NO:X" was often generated by overlapping sequences contained in multiple clones (contig analysis). A representative clone containing all or most of the sequence for SEQ ID NO:X is deposited at Human Genome Sciences, Inc. (HGS) in a catalogued and archived library. As shown in column 9 of Table 1, each clone is identified by a cDNA Clone ID. Each Clone ID is unique to an individual clone and the Clone ID is all the information needed to retrieve a given clone from the HGS library. In addition to the individual cDNA clone deposits, most of the cDNA libraries from which the clones were derived were deposited at the American Type Culture Collection (hereinafter "ATCC"). Table 5 provides a list of the deposited cDNA libraries. One can use the Clone ID to determine the library source by reference to Tables 2 and 5. Table 5 lists the deposited cDNA libraries by name and links each library to an ATCC Deposit. Library names contain four characters, for example, "HTWE." The name of a cDNA clone ("Clone ID") isolated from that library begins with the same four characters, for example "HTWEP07". As mentioned below, Table 1 correlates the Clone ID names with SEQ ID NOs. Thus, starting with a SEQ ID NO, one can use Tables 1, 2 and 5 to determine the corresponding Clone ID, from which library it came and in which ATCC deposit the library is contained. Furthermore, it is possible to retrieve a given cDNA clone from the source library by techniques known in the art and described elsewhere herein. The ATCC is located at 10801 University Boulevard, Manassas, Virginia 20110-2209, USA. The ATCC deposits were made persuant to the terms of the Budapest Treaty on the international recognition of the deposit of microorganisms for the purposes of patent procedure.

A "polynucleotide" of the present invention also includes those polynucleotides capable of hybridizing, under stringent hybridization conditions, to sequences contained in SEQ ID NO:X, or the complement thereof (e.g., the complement of any one, two, three, four, or more of the polynucleotide fragments described herein), and/or sequences contained in the related cDNA clone within a library deposited with the ATCC. "Stringent hybridization conditions" refers to an overnight incubation at 42 degree C in a solution comprising 50% formamide, 5x SSC (750 mM NaCl, 75 mM trisodium citrate), 50 mM sodium phosphate (pH

7.6), 5x Denhardt's solution, 10% dextran sulfate, and 20 µg/ml denatured, sheared salmon sperm DNA, followed by washing the filters in 0.1x SSC at about 65 degree C.

Also included within "polynucleotides" of the present invention are nucleic acid molecules that hybridize to the polynucleotides of the present invention at lower stringency hybridization conditions. Changes in the stringency of hybridization and signal detection are primarily accomplished through the manipulation of formamide concentration (lower percentages of formamide result in lowered stringency); salt conditions, or temperature. For example, lower stringency conditions include an overnight incubation at 37 degree C in a solution comprising 6X SSPE (20X SSPE = 3M NaCl; 0.2M NaH_2PO_4; 0.02M EDTA, pH 7.4), 0.5% SDS, 30% formamide, 100 ug/ml salmon sperm blocking DNA; followed by washes at 50 degree C with 1XSSPE, 0.1% SDS. In addition, to achieve even lower stringency, washes performed following stringent hybridization can be done at higher salt concentrations (e.g. 5X SSC).

Note that variations in the above conditions may be accomplished through the inclusion and/or substitution of alternate blocking reagents used to suppress background in hybridization experiments. Typical blocking reagents include Denhardt's reagent, BLOTTO, heparin, denatured salmon sperm DNA, and commercially available proprietary formulations. The inclusion of specific blocking reagents may require modification of the hybridization conditions described above, due to problems with compatibility.

Of course, a polynucleotide which hybridizes only to polyA+ sequences (such as any 3' terminal polyA+ tract of a cDNA shown in the sequence listing), or to a complementary stretch of T (or U) residues, would not be included in the definition of "polynucleotide," since such a polynucleotide would hybridize to any nucleic acid molecule containing a poly (A) stretch or the complement thereof (e.g., practically any double-stranded cDNA clone generated using oligo dT as a primer).

The polynucleotides of the present invention can be composed of any polyribonucleotide or polydeoxribonucleotide, which may be unmodified RNA or DNA or modified RNA or DNA. For example, polynucleotides can be composed of single- and double-stranded DNA, DNA that is a mixture of single- and double-stranded regions, single- and double-stranded RNA, and RNA that is mixture of single- and double-stranded regions, hybrid molecules comprising DNA and RNA that may be single-stranded or, more typically, double-stranded or a mixture of single- and double-stranded regions. In addition, the

polynucleotide can be composed of triple-stranded regions comprising RNA or DNA or both RNA and DNA. A polynucleotide may also contain one or more modified bases or DNA or RNA backbones modified for stability or for other reasons. "Modified" bases include, for example, tritylated bases and unusual bases such as inosine. A variety of modifications can be made to DNA and RNA; thus, "polynucleotide" embraces chemically, enzymatically, or metabolically modified forms.

In specific embodiments, the polynucleotides of the invention are at least 15, at least 30, at least 50, at least 100, at least 125, at least 500, or at least 1000 continuous nucleotides but are less than or equal to 300 kb, 200 kb, 100 kb, 50 kb, 15 kb, 10 kb, 7.5kb, 5 kb, 2.5 kb, 2.0 kb, or 1 kb, in length. In a further embodiment, polynucleotides of the invention comprise a portion of the coding sequences, as disclosed herein, but do not comprise all or a portion of any intron. In another embodiment, the polynucleotides comprising coding sequences do not contain coding sequences of a genomic flanking gene (i.e., 5' or 3' to the gene of interest in the genome). In other embodiments, the polynucleotides of the invention do not contain the coding sequence of more than 1000, 500, 250, 100, 50, 25, 20, 15, 10, 5, 4, 3, 2, or 1 genomic flanking gene(s).

"SEQ ID NO:X" refers to a tissue specific cancer antigen polynucleotide sequence described in Table 1. SEQ ID NO:X is identified by an integer specified in column 1 of Table 1. The polypeptide sequence SEQ ID NO:Y is a translated open reading frame (ORF) encoded by polynucleotide SEQ ID NO:X. There are 842 cancer antigen polynucleotide sequences described in Table 1 and shown in the sequence listing (SEQ ID NO:1 through SEQ ID NO:842). Likewise there are 842 polypeptide sequences shown in the sequence listing, one polypeptide sequence for each of the polynucleotide sequences (SEQ ID NO:843 through SEQ ID NO:1684). The polynucleotide sequences are shown in the sequence listing immediately followed by all of the polypeptide sequences. Thus, a polypeptide sequence corresponding to polynucleotide sequence SEQ ID NO:1 is the first polypeptide sequence shown in the sequence listing. The second polypeptide sequence corresponds to the polynucleotide sequence shown as SEQ ID NO:2, and so on. In otherwords, since there are842 polynucleotide sequences, for any polynucleotide sequence SEQ ID NO:X, a corresponding polypeptide SEQ ID NO:Y can be determined by the formula X + 842 = Y. In addition, any of the unique "Sequence/Contig ID" defined in column 2 of Table 1, can be linked to the corresponding polypeptide SEQ ID NO:Y by reference to Table 4.

The polypeptides of the present invention can be composed of amino acids joined to each other by peptide bonds or modified peptide bonds, i.e., peptide isosteres, and may contain amino acids other than the 20 gene-encoded amino acids. The polypeptides may be modified by either natural processes, such as posttranslational processing, or by chemical modification techniques which are well known in the art. Such modifications are well described in basic texts and in more detailed monographs, as well as in a voluminous research literature. Modifications can occur anywhere in a polypeptide, including the peptide backbone, the amino acid side-chains and the amino or carboxyl termini. It will be appreciated that the same type of modification may be present in the same or varying degrees at several sites in a given polypeptide. Also, a given polypeptide may contain many types of modifications. Polypeptides may be branched, for example, as a result of ubiquitination, and they may be cyclic, with or without branching. Cyclic, branched, and branched cyclic polypeptides may result from posttranslation natural processes or may be made by synthetic methods. Modifications include acetylation, acylation, ADP-ribosylation, amidation, covalent attachment of flavin, covalent attachment of a heme moiety, covalent attachment of a nucleotide or nucleotide derivative, covalent attachment of a lipid or lipid derivative, covalent attachment of phosphotidylinositol, cross-linking, cyclization, disulfide bond formation, demethylation, formation of covalent cross-links, formation of cysteine, formation of pyroglutamate, formylation, gamma-carboxylation, glycosylation, GPI anchor formation, hydroxylation, iodination, methylation, myristoylation, oxidation, pegylation, proteolytic processing, phosphorylation, prenylation, racemization, selenoylation, sulfation, transfer-RNA mediated addition of amino acids to proteins such as arginylation, and ubiquitination. (See, for instance, PROTEINS - STRUCTURE AND MOLECULAR PROPERTIES, 2nd Ed., T. E. Creighton, W. H. Freeman and Company, New York (1993); POSTTRANSLATIONAL COVALENT MODIFICATION OF PROTEINS, B. C. Johnson, Ed., Academic Press, New York, pgs. 1-12 (1983); Seifter et al., Meth Enzymol 182:626-646 (1990); Rattan et al., Ann NY Acad Sci 663:48-62 (1992).)

The cancer polypeptides of the invention can be prepared in any suitable manner. Such polypeptides include isolated naturally occurring polypeptides, recombinantly produced polypeptides, synthetically produced polypeptides, or polypeptides produced by a combination of these methods. Means for preparing such polypeptides are well understood in the art.

The polypeptides may be in the form of the secreted protein, including the mature form, or may be a part of a larger protein, such as a fusion protein (see below). It is often advantageous to include an additional amino acid sequence which contains secretory or leader sequences, pro-sequences, sequences which aid in purification, such as multiple histidine residues, or an additional sequence for stability during recombinant production.

The cancer polypeptides of the present invention are preferably provided in an isolated form, and preferably are substantially purified. A recombinantly produced version of a polypeptide, including the secreted polypeptide, can be substantially purified using techniques described herein or otherwise known in the art, such as, for example, by the one-step method described in Smith and Johnson, Gene 67:31-40 (1988). Polypeptides of the invention also can be purified from natural, synthetic or recombinant sources using techniques described herein or otherwise known in the art, such as, for example, antibodies of the invention raised against the polypeptides of the present invention in methods which are well known in the art.

By a polypeptide demonstrating a "functional activity" is meant, a polypeptide capable of displaying one or more known functional activities associated with a full-length (complete) protein of the invention. Such functional activities include, but are not limited to, biological activity, antigenicity [ability to bind (or compete with a polypeptide for binding) to an anti-polypeptide antibody], immunogenicity (ability to generate antibody which binds to a specific polypeptide of the invention), ability to form multimers with polypeptides of the invention, and ability to bind to a receptor or ligand for a polypeptide.

"A polypeptide having functional activity" refers to polypeptides exhibiting activity similar, but not necessarily identical to, an activity of a polypeptide of the present invention, including mature forms, as measured in a particular assay, such as, for example, a biological assay, with or without dose dependency. In the case where dose dependency does exist, it need not be identical to that of the polypeptide, but rather substantially similar to the dose-dependence in a given activity as compared to the polypeptide of the present invention (i.e., the candidate polypeptide will exhibit greater activity or not more than about 25-fold less and, preferably, not more than about tenfold less activity, and most preferably, not more than about three-fold less activity relative to the polypeptide of the present invention).

The functional activity of the cancer antigen polypeptides, and fragments, variants derivatives, and analogs thereof, can be assayed by various methods.

For example, in one embodiment where one is assaying for the ability to bind or compete with full-length polypeptide of the present invention for binding to an antibody to the full length polypeptide antibody, various immunoassays known in the art can be used, including but not limited to, competitive and non-competitive assay systems using techniques such as radioimmunoassays, ELISA (enzyme linked immunosorbent assay), "sandwich" immunoassays, immunoradiometric assays, gel diffusion precipitation reactions, immunodiffusion assays, in situ immunoassays (using colloidal gold, enzyme or radioisotope labels, for example), western blots, precipitation reactions, agglutination assays (e.g., gel agglutination assays, hemagglutination assays), complement fixation assays, immunofluorescence assays, protein A assays, and immunoelectrophoresis assays, etc. In one embodiment, antibody binding is detected by detecting a label on the primary antibody. In another embodiment, the primary antibody is detected by detecting binding of a secondary antibody or reagent to the primary antibody. In a further embodiment, the secondary antibody is labeled. Many means are known in the art for detecting binding in an immunoassay and are within the scope of the present invention.

In another embodiment, where a ligand is identified, or the ability of a polypeptide fragment, variant or derivative of the invention to multimerize is being evaluated, binding can be assayed, e.g., by means well-known in the art, such as, for example, reducing and non-reducing gel chromatography, protein affinity chromatography, and affinity blotting. See generally, Phizicky, E., et al., Microbiol. Rev. 59:94-123 (1995). In another embodiment, physiological correlates polypeptide of the present invention binding to its substrates (signal transduction) can be assayed.

In addition, assays described herein (see Examples) and otherwise known in the art may routinely be applied to measure the ability of polypeptides of the present invention and fragments, variants derivatives and analogs thereof to elicit polypeptide related biological activity (either in vitro or in vivo). Other methods will be known to the skilled artisan and are within the scope of the invention.

<u>Cancer Associated Polynucleotides and Polypeptides of the Invention</u>

It has been discovered herein that the polynucleotides described in Table 1 are expressed at significantly enhanced levels in human cancer tissues as shown in column 10 of

Table 1. Accordingly, such polynucleotides, polypeptides encoded by such polynucleotides, and antibodies specific for such polypeptides find use in the prediction, diagnosis, prevention and treatment of tissue specific disorders, including cancer as more fully described below.

Table 1 summarizes some of the polynucleotides encompassed by the invention (including contig sequences (SEQ ID NO:X) and the related cDNA clones) and further summarizes certain characteristics of these tissue specific cancer associated polynucleotides and the polypeptides encoded thereby.

Table 1

Seq ID No.	Sequence/ Contig ID	Gene Name	Overlap	HGS Nucleotide Start	End	% Identity	% Similarity	Clone ID	Tissue(s)
1	507291	uvomorulin [Homo sapiens] >sp|Q15855|Q15855 UVOMORULIN PRECURSOR (E-CADHERIN) (ARC-1/UVOMORULIN). >gi|930046 uvomorulin (140 AA) [Homo sapiens] {SUB 168-307} Length = 878	gi|340185	2	475	100	100	HCHAU23	Pancreas. Breast/Ovarian
2	508000	HLA-B-associated transcript 2 (BAT2) [Homo sapiens] >gi|179345 HLA-B-associated transcript 2 (BAT2) [Homo sapiens] >pir|B35098|B35098 MHC class III histocompatibility antigen HLA-B-associated transcript 2 - human >sp|P48634|BAT2_HUMAN LARGE PROLINE-RICH P	gi|179339	100	1902	86	87	HWAAK56	Lung. Breast/Ovarian
3	518325			110	310			HHFCP36	Lung. Pancreas. Colon. Breast/Ovarian
4	523111	Sm D2 [Homo sapiens] >pir|I38861|I38861 small nuclear ribonucleoprotein chain D2 - human Length = 118	gi|600748	233	670	88	88	HATAE67	Lung. Breast/Ovarian
5	526869	(AC002291) Similar ATP-dependent RNA Helicase [Arabidopsis thaliana] >sp|O49289|O49289 SIMILAR ATP-DEPENDENT RNA HELICASE. Length = 845	gi|2829912	1	552	67	77	HT4FP57	Pancreas. Breast/Ovarian
6	532211	retinoic acid-binding protein [Bos taurus] Length = 138	gi|162906	2	481	95	98	HHGCV63	Lung. Breast/Ovarian

7	532247			160	384			HEBCC47	Pancreas. Breast/Ovarian
8	537932	alcohol dehydrogenase [Homo sapiens] >gi|178134 alcohol dehydrogenase 3 [Homo sapiens] >pir|JH0789|DEHUC2 alcohol dehydrogenase (EC 1.1.1.1) 5 - human >sp|P11766|ADHX_HUMAN ALCOHOL DEHYDROGENASE CLASS III CHI CHAIN (EC 1.1.1.1) (GLUTATHIONE-DEPENDENT FOR	gi|178130	1	1149	92	92	HUSIB86	Lung. Breast/Ovarian
9	540117			174	635			HRGBU25	Lung. Breast/Ovarian
10	547710	transketolase [Homo sapiens] Length = 623	gi|1297297	2	1189	92	92	HMUAZ27	Lung. Pancreas
11	551747	rtvp-1 [Homo sapiens] >pir|JC5308|JC5308 testis-specific, vespid, and pathogenesis-related protein 1 - human >sp|P48060|GLIP_HUMAN GLIOMA PATHOGENESIS-RELATED PROTEIN (RTVP-1 PROTEIN). Length = 266	gi|1030053	26	931	91	91	HTDAE10	Lung. Pancreas
12	552799	delta- aminolevulinate synthase (housekeeping) [Homo sapiens] >pir|S13682|SYHUAL 5-aminolevulinate synthase (EC 2.3.1.37) 1 precursor - human >sp|P13196|HEM1_HUMAN 5-AMINOLEVULINIC ACID SYNTHASE MITOCHONDRIAL PRECURSOR, NONSPECIFIC (EC 2.3.1.37) (DELTA-AM	gi|28583	104	814	100	100	HHECX90	Lung. Pancreas. Breast/Ovarian

13	553243	RING7 [Homo sapiens] >gi|557702 HLA-DMB [Homo sapiens] >gi|512472 HLA-DMB [Homo sapiens] >gi|1054742 DMB [Homo sapiens] >pir|I37533|I37533 MHC class II histocompatibility antigen HLA-DM beta chain precursor - human Length = 263	gi|313002	202	1017	93	93	HUKDI44	Lung, Pancreas
14	553368	(AF053944) aortic carboxypeptidase-like protein ACLP [Homo sapiens] >sp|G3288916|G3288916 AORTIC CARBOXYPEPTIDASE-LIKE PROTEIN ACLP. >gnl|PID|d1013781 AEBP1 [Homo sapiens] {SUB 314-1158} Length = 1158	gi|3288916	1	459	96	96	HADGE84	Lung, Pancreas
15	554349			3	776			HUSGK19	Lung, Pancreas
16	558491	immunoglobulin heavy chain [Homo sapiens] Length = 152	gi|567128	1	429	98	100	HUFCN61	Lung, Pancreas, Colon
17	558983	dJ68O2.2 [Homo sapiens] >sp|P35579|MYSN_HUMAN MYOSIN HEAVY CHAIN, NONMUSCLE TYPE A (CELLULAR MYOSIN HEAVY CHAIN, TYPE A) (NMMHC-A). >gi|553596 cellular myosin heavy chain [Homo sapiens] {SUB 1-1337} Length = 1960	gnl|PID|e1294465	219	623	100	100	HOHBM82	Pancreas, Breast/Ovarian
18	572943			367	522			HBAMC47	Pancreas, Breast/Ovarian
19	585892	epithelial tumor antigen precursor, membrane-bound form - human Length = 515	pir|S10572|S10572	3	965	89	89	HUKAL69	Lung, Pancreas, Colon, Breast/Ovarian

20	589390	C1 inhibitor [Homo sapiens] >gi|29535 C1 inhibitor [Homo sapiens] >pir|S15386|ITHUC1 complement C1 inhibitor precursor - human >sp|P05155|IC1_HUMAN PLASMA PROTEASE C1 INHIBITOR PRECURSOR (C1 INH). >gnl|PID|e3783 C1 inhibitor (AA 155-478) (1 is 2nd base i	gnl|PID|e222400	3	983	96	96	HSRAB10	Lung, Pancreas
21	596882			800	1057			HMCEP91	Lung, Pancreas, Colon
22	616289	nucleoporin p58 [Rattus norvegicus] >sp|P70581|P70581 NUCLEOPORIN P58. Length = 585	gi|1537068	1	390	67	70	HAJCB44	Lung, Pancreas
23	622140	selenophosphate synthetase 2 [Homo sapiens] >sp|Q99611|Q99611 SELENOPHOSPHATE SYNTHETASE 2. Length = 448	gi|1815622	92	325	97	97	HEONC67	Pancreas, Breast/Ovarian
24	623566	karyopherin alhph 3 [Homo sapiens] >sp|O00505|IMA3_HUMAN IMPORTIN ALPHA-3 SUBUNIT (KARYOPHERIN ALPHA-3 SUBUNIT). Length = 521	gnl|PID|d1021210	66	1652	99	99	HDPPP20	Lung, Breast/Ovarian
25	647714			1	711			HSSEH29	Pancreas, Breast/Ovarian
26	647752	ubiquitin conjugating-protein [Oryctolagus cuniculus] >gi|184046 HHR6B (Human homologue of yeast RAD 6); putative [Homo sapiens] >gi|30954 E2 protein [Homo sapiens] >gi|207555 ubiquitin conjugating-protein [Rattus norvegicus] >gnl|PID|e233515 HR6B gene pr	gi|165780	3	590	100	100	HDTDH46	Lung, Colon

27	651774	P58 [Homo sapiens] >pir|S68363|S68363 protein disulfide-isomerase (EC 5.3.4.1) ER60 precursor - human >sp|P30101|ER60_HUMAN PROBABLE PROTEIN DISULFIDE ISOMERASE ER-60 PRECURSOR (EC 5.3.4.1) (ERP60) (58 KD MICROSOMAL PROTEIN) (P58) (GRP58) (ERP57). Length	gi|1147739	1	1632	96	96	HDPAA15	Lung, Pancreas. Breast/Ovarian
28	651995	collagen [Mus musculus] >pir|S23779|S23779 collagen alpha 1(VIII) chain - mouse >sp|Q00780|CA18_MOUSE COLLAGEN ALPHA 1(VIII) CHAIN PRECURSOR. >bbs|134935 alpha 1-VIII collagen [rats, mesangial cell, Peptide Partial, 172 aa] [Rattus sp.] {SUB 399-570} Leng	gnl|PID|e245912	3	335	90	95	HBTAD44	Lung, Pancreas
29	652156	phospholipid hydroperoxide glutathione peroxidase [Homo sapiens] >sp|O43381|O43381 GSHH_HUMAN (EC 1.11.1.9) (GLUTATHIONE PEROXIDASE). >gi|3399677 (AC005390) GSSH_HUMAN, partial CDS [Homo sapiens] {SUB 149-197} Length = 197	gi|825667	262	633	94	94	HOEBK80	Lung. Breast/Ovarian
30	653010			79	183			HSRAA58	Lung, Pancreas
31	655904	von Willebrand factor [Homo sapiens] >pir|A34480|VWHU von Willebrand factor precursor - human >gi|553810 von Willebrand factor [Homo sapiens] {SUB 990-1947} >gnl|PID|e222518 von Willebrand factor [Homo sapiens] {SUB 1-178} >gi|340316 von Willebrand antige	gi|340356	632	1891	96	96	HSEBB94	Lung. Breast/Ovarian
32	657852			70	522			HCHAL14	Colon. Breast/Ovarian
33	666414			1	285			HOSFG18	Lung, Pancreas

34	667847	ribosomal protein S9 [Rattus norvegicus] >pir|JN0587|S21497 ribosomal protein S9 - rat Length = 194	gi|57143	1	714	98	98	HCFLJ62	Lung, Pancreas, Breast/Ovarian
35	670188	G protein gamma-10 subunit [Homo sapiens] >pir|I39158|I39158 GTP-binding regulatory protein gamma-10 chain - human >sp|P50151|GBGA_HUMAN GUANINE NUCLEOTIDE-BINDING PROTEIN G(I)/G(S)/G(O) GAMMA-10 SUBUNIT. Length = 68	gi|995919	2	238	100	100	HWADR30	Lung, Pancreas
36	670279	ribosomal protein S24 [Homo sapiens] >gi|517222 ribosomal protein S24 [Homo sapiens] >gi|49652 ribosomal protein S19 (AA 1 - 133) [Mesocricetus auratus] >gi|57858 ribosomal protein S24 [Rattus norvegicus] >gi|57722 ribosomal protein S24 (AA 1-133) [Rattus	gi|337506	96	503	87	87	HSAYG46	Lung, Pancreas, Breast/Ovarian
37	670729	acidic ribosomal phosphoprotein (P1) [Homo sapiens] >pir|B27125|R6HUP1 acidic ribosomal protein P1 - human Length = 114	gi|190234	74	496	100	100	H2CBM17	Lung, Pancreas, Colon, Breast/Ovarian
38	674123			40	438			HYACJ55	Lung, Pancreas
39	676496	collagen type VI, alpha 3 chain [Homo sapiens] >sp|E1292418|E1292418 COLLAGEN TYPE VI, ALPHA 3 CHAIN. Length = 3176	gnl|PID|e1292418	250	1029	98	98	HSLIC82	Lung, Pancreas
40	678162	TAXREB107 [Homo sapiens] >pir|I51803|I51803 TAXREB107 - human Length = 288	gnl|PID|d1005017	528	974	100	100	HBJJA02	Lung, Pancreas, Breast/Ovarian

41	678248	dolichol-phosphate-mannose synthase [Homo sapiens] >sp|O60762|O60762 DOLICHOL-PHOSPHATE-MANNOSE SYNTHASE. >gnl|PID|d1026578 dolichol-phosphate-mannose synthase [Homo sapiens] {SUB 1-120} Length = 260	gnl|PID|d1026577	3	770	100	100	HMTAK71	Lung, Pancreas
42	683668	alpha 1 (I) chain propeptide [Homo sapiens] >gi|180380 alpha-1 type I collagen [Homo sapiens] {SUB 64-201} Length = 1040	gi|180392	566	1912	94	94	HWHGV07	Lung, Pancreas, Breast/Ovarian
43	693172	Q1Z 7F5 [Homo sapiens] >gi|189266 may code for Wilm's tumor-related protein [Homo sapiens] >gi|190814 Wilm's tumor-related protein [Homo sapiens] >gi|1203971 QM gene product [Homo sapiens] >bbs|135740 QM [human, nontumorigenic Wilms' microcell hybrid c	gi|184407	23	214	97	100	HNHIW05	Lung, Pancreas, Breast/Ovarian
44	694303			2824	3219			HOGAV47	Lung, Breast/Ovarian
45	695042	Description: KRAB zinc finger protein; this is a splicing variant that contains a stop codon and frame shift between the KRAB box and the zinc finger region; Method: conceptual translation supplied by author [Homo sapiens] >sp|Q13359|Q13359 KRAB ZINC FING	gi|1049295	471	680	74	91	HISBX26	Pancreas, Breast/Ovarian
46	699799	lipocortin (AA 1-346) [Homo sapiens] >pir|A03080|LUHU annexin I - human >sp|P04083|ANX1_HUMAN ANNEXIN I (LIPOCORTIN I) (CALPACTIN II) (CHROMOBINDIN 9) (P35) (PHOSPHOLIPASE A2 INHIBITORY PROTEIN). {SUB 2-346} Length = 346	gi|34388	3	1121	100	100	HNDAA51	Lung, Breast/Ovarian

47	702216	dihydrodiol dehydrogenase [Homo sapiens] >gi|487135 hepatic dihydrodiol dehydrogenase [Homo sapiens] >gi|181549 dihydrodiol dehydrogenase [Homo sapiens] >pir|A53436|A53436 3-alpha-hydroxysteroid/dihydrodiol dehydrogenase (EC 1.1.1.-) - human >sp|Q04828|DB	gi|452484	41	1048	95	95	HNALC11	Lung, Pancreas
48	703015	latent transforming growth factor-beta-binding protein - human Length = 1820	pir|A55494|A55494	3	587	100	100	HGCOX28	Lung, Pancreas
49	706391	vacuolar H+ ATPase proton channel subunit [Homo sapiens] >pir|A39367|A39367 H+-transporting ATPase (EC 3.6.1.35) chain PKD1 - human Length = 155	gi|189676	29	622	85	85	HMABL73	Lung, Breast/Ovarian
50	706892	copper transport protein HAH1 [Homo sapiens] >sp|O00244|O00244 COPPER TRANSPORT PROTEIN HAH1. Length = 68	gi|1945365	3	287	82	82	HUFDS83	Lung, Breast/Ovarian
51	706924			2847	3215			HRAEB20	Lung, Breast/Ovarian
52	707642	ribosomal protein L8 [Homo sapiens] >gi|57704 ribosomal protein L8 [Rattus rattus] >gi|1527178 ribosomal protein L8 [Mus musculus] >pir|JU0177|R5RTL8 ribosomal protein L8, cytosolic - rat >pir|JN0923|JN0923 ribosomal protein L8, cytosolic - human >gi|3851	gi|433899	1	516	94	94	HSRDJ44	Lung, Pancreas, Colon, Breast/Ovarian
53	710369			99	611			HSPA18	Lung, Pancreas, Breast/Ovarian
54	718826			581	877			HSIFK68	Lung, Breast/Ovarian

55	719790	lipocortin II [Homo sapiens] >pir|A23942|LUHU36 annexin II - human >sp|P07355|ANX2_HUMAN ANNEXIN II (LIPOCORTIN II) (CALPACTIN I HEAVY CHAIN) (CHROMOBINDIN 8) (P36) (PROTEIN I) (PLACENTAL ANTICOAGULANT PROTEIN IV) (PAP-IV). {SUB 2-339} >sp|G545587|G545587	gnl|PID|d1000439	3	869	98	98	HKABK62	Lung, Pancreas
56	720222	homology with 16.7 KD putative viral protein YUB1_NPVAC [Caenorhabditis elegans] Length = 250	gnl|PID|e1346018	34	729	45	60	HSKEP04	Lung, Pancreas, Breast/Ovarian
57	724033			1	654			HPJBV92	Lung, Pancreas, Breast/Ovarian
58	724767	epsilon isoform of 61kDa regulatory subunit of PP2A [Homo sapiens] >gi|1478070 protein phosphatase B56-epsilon [Homo sapiens] >sp|Q16537|Q16537 EPSILON ISOFORM OF 61KDA REGULATORY SUBUNIT OF PP2A. >gi|1022892 protein phosphatase PP2A0 B' subunit delta is	gnl|PID|e220196	71	526	100	100	HKABH59	Lung, Breast/Ovarian
59	727065	ATPase [Homo sapiens] Length = 617	gi|291868	228	1010	99	99	HELGY15	Lung, Pancreas
60	727246	(AB009282) cytochrome b5 [Homo sapiens] >sp|O43169|O43169 CYTOCHROME B5 (FRAGMENT). Length = 146	gnl|PID|d1024640	3	509	96	98	HCFMH52	Lung, Colon
61	727932			41	199			HLJDO53	Lung, Breast/Ovarian
62	731167	Sec23 protein [Homo sapiens] Length = 765	gnl|PID|e236013	1	987	99	99	HDTEM51	Lung, Pancreas

63	732514	lysophosphatidic acid acyltransferase-alpha [Homo sapiens] >gi|2253613 putative lysophospholipid acyltransferase [Homo sapiens] >gnl|PID|e286645 1-acylglycerol-3-phosphate O-acyltransferase [Homo sapiens] >sp|Q99943|PLCA_HUMAN 1-ACYL-SN-GLYCEROL-3-PHOSPHA	gi|2155238	3	794	99	99	HLDBX26	Pancreas, Prostate
64	734080			1	567			HFIBK44	Lung, Breast/Ovarian
65	734288	cysteinyl-tRNA synthetase [Homo sapiens] Length = 595	gi|927229	154	2067	99	99	HKABU01	Lung, Pancreas
66	739448	Nascent polypeptide associated complex alpha subunit [Homo sapiens] >gi|4092060 (AF054187) alpha NAC [Homo sapiens] >pir|S49326|S49326 Nascent polypeptide associated complex alpha chain - human >sp|Q13765|Q13765 NASCENT POLYPEPTIDE ASSOCIATED COMPLEX ALPH	gi|556642	441	1184	82	82	HKGAT31	Lung, Breast/Ovarian
67	739668			2	484			HAPTL07	Lung, Pancreas
68	740060	Diff33 gene product [Homo sapiens] >sp|Q13530|Q13530 PLACENTAL PROTEIN DIFF33. Length = 494	gi|1293563	76	1536	94	94	HMEGB82	Lung, Pancreas
69	741560			3	296			HCGMI12	Lung, Colon
70	742543	human gamma-glutamyl hydrolase [Homo sapiens] >sp|Q92820|Q92820 HUMAN GAMMA-GLUTAMYL HYDROLASE (EC 3.4.22.12). Length = 318	gi|2951931	187	804	99	100	HE2BG62	Lung, Colon, Breast/Ovarian
71	742831			25	297			HCDAL47	Pancreas, Colon

72	745327	channel-like integral membrane protein [Homo sapiens] >gi|1314304 channel-like integral membrane protein [Homo sapiens] >pir|A41616|A41616 erythrocyte integral membrane protein 28K - human >sp|P29972|AQP1_HUMAN AQUAPORIN-CHIP (WATER CHANNEL PROTEIN FOR RE	gi|180501	1	534	98	98	HWHPM73	Lung, Pancreas
73	745695	Mac-2 binding protein [Homo sapiens] >gi|483474 90K gene product [Homo sapiens] >pir|A47161|A47161 Mac-2-binding glycoprotein precursor - human >sp|Q08380|Q08380 MAC-2 BINDING PROTEIN PRECURSOR. Length = 585	gi|307153	886	2016	98	98	HOPBN02	Lung, Pancreas
74	750316	(AF029890) hepatitis B virus X interacting protein [Homo sapiens] >sp|O43504|O43504 HEPATITIS B VIRUS X INTERACTING PROTEIN. Length = 91	gi|2745883	99	398	100	100	HKMLD65	Lung, Pancreas, Breast/Ovarian
75	750522			172	906			HUKFI58	Lung, Pancreas, Colon, Breast/Ovarian
76	750583			58	189			HBJJB66	Lung, Breast/Ovarian
77	751020			1	480			HEBAE80	Lung, Breast/Ovarian
78	752196			1	120			HL1AL67	Pancreas, Prostate
79	753084	UGTrel1 [Homo sapiens] >pir|JC5024|JC5024 UDP-galactose transporter related isozyme 1 - human >sp|P78383|P78383 UGTREL1. Length = 322	gi|1669560	53	1168	87	87	HDPKG74	Lung, Pancreas
80	754957	The ha1237 gene product is related to S.pombe rad21 gene product. [Homo sapiens] Length = 631	gnl|PID|d1008135	242	1330	94	94	HWBGB01	Lung, Pancreas

81	756557	myosin I heavy chain [Rattus norvegicus] >pir|A45439|A45439 myosin I heavy chain - rat >sp|Q05096|Q05096 MYOSIN HEAVY CHAIN 1. Length = 1136	gi|56733	1	888	94	94	HE8AF67	Lung, Pancreas. Colon. Breast/Ovarian
82	756712			1457	1729			HSYBW76	Lung. Pancreas
83	757414	5-lipoxygenase activating protein [Homo sapiens] >pir|A39824|A39824 5-lipoxygenase-activating protein - human >sp|P20292|FLAP_HUMAN 5-LIPOXYGENASE ACTIVATING PROTEIN (FLAP) (MK-886-BINDING PROTEIN). Length = 161	gi|182658	1	477	99	100	HCABA08	Lung. Colon
84	757614	tetratricopeptide repeat protein [Homo sapiens] >sp|Q99614|Q99614 TETRATRICOPEPTIDE REPEAT PROTEIN. Length = 292	gi|1688074	83	991	100	100	HMEJS13	Lung, Pancreas. Breast/Ovarian
85	757815	(AF038604) contains similarity to Drosophila ovarian tumor locus protein (GB:X13693) [Caenorhabditis elegans] >sp|O44438|O44438 B0546.2 PROTEIN. Length = 346	gi|2702370	2	988	58	81	HCHOL74	Lung. Breast/Ovarian
86	759878	nuclear pore complex protein NUP107 [Rattus norvegicus] >pir|A54142|A54142 nucleoporin NUP107 - rat >sp|P52590|N107_RAT NUCLEAR PORE COMPLEX PROTEIN NUP107 (NUCLEOPORIN NUP107) (107 KD NUCLEOPORIN) (P105). Length = 926	gi|510717	526	1833	86	88	HNTAP78	Lung. Breast/Ovarian
87	760227	(AC003040) putative nicotinate phosphoribosyltransferase [Arabidopsis thaliana] >sp|O80459|O80459 PUTATIVE NICOTINATE PHOSPHORIBOSYLTRANSFERASE. Length = 574	gi|3242705	2	484	52	71	HCHMM71	Pancreas. Breast/Ovarian

88	760312	chondroitin sulfate proteoglycan versican V0 splice-variant precursor peptide [Homo sapiens] >sp|P13611|PGCV_HUMAN VERSICAN CORE PROTEIN PRECURSOR (LARGE FIBROBLAST PROTEOGLYCAN) (CHONDROITIN SULFATE PROTEOGLYCAN CORE PROTEIN 2) (GLIAL HYALURONATE- BINDIN	gi|608515	993	3215	99	99	HMVDD07	Lung, Pancreas
89	766051			1	627			HMAFA79	Lung, Breast/Ovarian
90	767593			327	497			HCECT76	Pancreas, Colon
91	768053	(AF039688) antigen NY-CO-3 [Homo sapiens] >sp|O60525|O60525 ANTIGEN NY-CO-3 (FRAGMENT). Length = 192	gi|3170176	251	625	99	99	HTPEH71	Pancreas, Breast/Ovarian
92	768055	ATP synthase gamma-subunit [Homo sapiens] >gnl|PID|d1004512 ATP synthase gamma-subunit [Homo sapiens] >pir|A49108|A49108 H+-transporting ATP synthase (EC 3.6.1.34) gamma chain - human >sp|P36542|ATPG_HUMAN ATP SYNTHASE GAMMA CHAIN, MITOCHONDRIAL PRECURSOR	gnl|PID|d1004511	32	949	100	100	HAJAQ70	Lung, Pancreas
93	769685	src-like tyrosine kinase (put.); putative [Homo sapiens] Length = 537	gi|338228	1005	1409	100	100	HRADN48	Lung, Pancreas, Colon, Breast/Ovarian
94	771920	F36D4.2 gene product [Caenorhabditis elegans] >sp|Q20100|Q20100 COSMID F36D4. Length = 224	gi|1245686	711	1562	58	77	HA1DT44	Lung, Pancreas
95	772790	cell division inhibitor [Synechocystis sp.] >pir|S77404|S77404 cell division inhibitor - Synechocystis sp. (PCC 6803) >sp|P73467|P73467 CELL DIVISION INHIBITOR. Length = 339	gnl|PID|d1018240	145	1158	35	54	HCEOT95	Lung, Breast/Ovarian

96	772916	similarto human ZFY protein. [Homo sapiens] >sp|Q92610|Q92610 MYELOBLAST KIAA0211. Length = 1267	gnl|PID|d1013891	3	965	99	99	HCEIT26	Lung. Pancreas
97	773225			52	504			HCLBI78	Lung. Pancreas
98	773632	Hrs [Homo sapiens] >gi|2731383 HGF receptor substrate Hrs [Homo sapiens] >sp|O14964|O14964 HRS, COMPLETE CDS. Length = 777	gnl|PID|d1024245	1	309	98	98	HCEVQ60	Pancreas. Prostate. Breast/Ovarian
99	774364	(AF080561) SYT interacting protein SIP [Homo sapiens] >sp|O75932|O75932 SYT INTERACTING PROTEIN SIP. Length = 669	gi|3746787	1	408	100	100	HCHAR77	Pancreas. Breast/Ovarian
100	775355			1599	1781			HDTBY31	Lung. Pancreas
101	775844	rfp transforming protein [Homo sapiens] >pir|A28101|TVHURF ret finger protein - human >gnl|PID|e308255 RFP [Homo sapiens] {SUB 250-513} Length = 513	gi|337372	138	1877	92	92	HISCU10	Lung, Pancreas
102	777760	(AF015040) NUMB protein [Homo sapiens] >sp|G4102705|G4102705 NUMB PROTEIN. >gi|4050088 (AF109907) S171 [Homo sapiens] {SUB 79-603} >gi|887362 ORF; putative [Homo sapiens] {SUB 469-603} Length = 603	gi|4102705	62	1372	88	88	HMSITK67	Pancreas. Breast/Ovarian
103	779837	tazarotene-induced gene 2 [Homo sapiens] >sp|Q99969|Q99969 TAZAROTENE-INDUCED GENE 2. Length = 163	gi|1848264	88	567	97	98	HSWBV38	Lung. Pancreas
104	780769	(AF084259) bromodomain-containing protein BP75 [Mus musculus] >sp|O88665|O88665 BROMODOMAIN-CONTAINING PROTEIN BP75. Length = 651	gi|3493162	100	762	35	58	HULBS08	Lung. Pancreas
105	781445			496	1443			HMVAP52	Pancreas. Breast/Ovarian

106	781531	lumican [Homo sapiens] Length = 338	gi|699577	1	486	100	100	HCHAF71	Pancreas. Breast/Ovarian
107	783018	ovary2 [Drosophila melanogaster] >sp|Q27924|Q27924 OVARY2. >gi|1208729 ovary2 [Drosophila melanogaster] {SUB 386-545} Length = 545	gi|1208732	120	674	58	76	HTPCZ45	Pancreas. Breast/Ovarian
108	783097	myogenic repressor I-mf [Homo sapiens] >sp|Q99750|Q99750 MYOGENIC REPRESSOR I-MF. Length = 246	gi|1763615	413	919	85	85	HMWGR19	Lung. Colon
109	784198	(AJ005893) JM26 [Homo sapiens] >sp|O60828|O60828 JM26 PROTEIN. COMPLETE CDS (CLONE LLOXNC01U138D3 (BAYLOR COLLEGE)). Length = 265	gnl|PID|e1289747	80	943	81	81	HNTNB85	Lung. Pancreas. Breast/Ovarian
110	784868	WW-domain binding protein 1 [Mus musculus] >sp|P97764|P97764 WW-DOMAIN BINDING PROTEIN 1. Length = 305	gi|1777577	1	969	77	85	HNTNQ08	Lung. Pancreas. Breast/Ovarian
111	785428	translation initiation factor 5 [Homo sapiens] >sp|P55010|IF5_HUMAN EUKARYOTIC TRANSLATION INITIATION FACTOR 5 (EIF-5). Length = 431	gi|1229140	308	1606	87	87	HPMCH4	Lung. Pancreas. Breast/Ovarian
112	785845			67	1350			HCGBE06	Lung. Colon. Breast/Ovarian
113	785854			3	509			HUSXJ65	Lung. Pancreas
114	786705			64	180			HBJJB89	Lung. Pancreas. Breast/Ovarian
115	787186			319	975			HUKBB89	Lung. Pancreas
116	787279	proteasome subunit z [Homo sapiens] >sp|Q99436|Q99436 PROTEASOME SUBUNIT Z. Length = 277	gnl|PID|d1007816	80	856	94	94	HKAJZ91	Lung. Breast/Ovarian
117	789002			178	402			HATBM56	Lung. Pancreas. Breast/Ovarian

118	789008	1.8 kb mRNA (AA 1-84) [Homo sapiens] >pir|S03384|S03384 hypothetical protein (IGF-II 3' region) - human >sp|P09565|IG2R_HUMAN PUTATIVE INSULIN-LIKE GROWTH FACTOR II ASSOCIATED PROTEIN. Length = 84	gi|33000	1354	1737	100	100	HISCN20	Lung, Pancreas
119	789555	(AL035247) hypothetical trp-asp repeat protein [Schizosaccharomyces pombe] Length = 760	gnl|PID|e1371207	124	1815	42	66	HTTCB23	Pancreas, Breast/Ovarian
120	789631			192	320			HLICN93	Lung, Pancreas, Colon
121	789779			1	396			HCHMS40	Colon, Breast/Ovarian
122	790387			3	527			HLMNA32	Colon, Breast/Ovarian
123	790461	(AF008445) phospholipid scramblase [Homo sapiens] >gnl|PID|d1033532 (AB006746) hMmTRA1b [Homo sapiens] >gi|4092081 (AF098642) phospholipid scramblase; plasma membrane phospholipid scramblase [Homo sapiens] >sp|O15162|O15162 PHOSPHOLIPID SCRAMBLASE. >sp|G4	gi|2282601	105	1193	99	99	HTGAV10	Lung, Pancreas, Breast/Ovarian
124	790931			2	394			HBCAO30	Pancreas, Breast/Ovarian
125	791176	(AB002107) hPer [Homo sapiens] >gi|2435507 (AF022991) Rigui [Homo sapiens] >sp|O15534|O15534 RIGUI. Length = 1290	dbj||AB002107_1	3	1034	90	90	HNFCJ67	Lung, Pancreas
126	791983			637	837			HBJLE45	Lung, Pancreas, Colon, Breast/Ovarian

127	792539	(AF020833) eukaryotic translation initiation factor 3 subunit [Homo sapiens] >sp|O14801|O14801 EUKARYOTIC TRANSLATION INITIATION FACTOR 3 SUBUNIT. Length = 320	gi|2460200	94	1068	94	94	HDPPX89	Lung, Pancreas, Breast/Ovarian
128	792749	protein arginine N-methyltransferase [Rattus norvegicus] >sp|Q63009|ANM1_RAT PROTEIN ARGININE N-METHYLTRANSFERASE 1 (EC 2.1.1.-). Length = 353	gi|1390025	34	1104	95	96	HDQEP64	Lung, Breast/Ovarian
129	792961	(AF036249) polymerase I-transcript release factor; PTRF [Mus musculus] >sp|O54724|O54724 POLYMERASE I AND TRANSCRIPT RELEASE FACTOR (POLYMERASE I-TRANSCRIPT RELEASE FACTOR). Length = 392	gi|2674195	778	1305	85	86	HMEKG25	Lung, Breast/Ovarian
130	793206	dJ1409.2 (Melanoma-Associated Antigen MAGE LIKE) [Homo sapiens] >sp|O76058|O76058 DJ1409.2 (MELANOMA-ASSOCIATED ANTIGEN MAGE LIKE). Length = 606	gn|PID|e1311294	889	1365	99	99	HTWFN71	Lung, Pancreas
131	793249	proliferation associated gene (pag) gene product [Homo sapiens] >pir|A46711|A46711 proliferation associated gene (pag) protein - human Length = 199	gi|287641	3	701	100	100	HJAAE81	Lung, Pancreas, Breast/Ovarian
132	793626	alpha mannosidase II isozyme [Homo sapiens] >sp|P49641|MA2X_HUMAN ALPHA-MANNOSIDASE IIX (EC 3.2.1.114) (MANNOSYL-OLIGOSACCHARIDE 1,3-1,6-ALPHA-MANNOSIDASE) (MAN IIX). Length = 1139	gn|PID|d1010153	119	640	99	99	HWABS13	Lung, Pancreas

133	794417	(AF047470) malate dehydrogenase precursor [Homo sapiens] >sp|O43682|O43682 MALATE DEHYDROGENASE (EC 1.1.1.37) PRECURSOR (EC 1.1.1.37). Length = 338	gi|2906146	3	1142	99	99	HFPBR03	Lung, Pancreas, Breast/Ovarian
134	795197			82	888			HDPFT26	Lung, Breast/Ovarian
135	795251	GAP SH3 binding protein [Homo sapiens] >sp|Q13283|Q13283 GAP SH3 BINDING PROTEIN. Length = 466	gi|1051170	101	1531	91	91	HE8FJ92	Pancreas, Breast/Ovarian
136	795752			2	1018			HWBDR92	Lung, Pancreas
137	796261	ubiquitin carrier protein E2 - human >gi|181916 ubiquitin carrier protein [Homo sapiens] {SUB 23-247} Length = 247	pir|B42856|B42856	3	851	87	87	HCHPQ06	Colon, Breast/Ovarian
138	796933	lumican [Homo sapiens] Length = 338	gi|699577	49	1107	94	94	HPMSD56	Lung, Pancreas, Prostate, Colon, Breast/Ovarian
139	799424			525	1553			HEONK47	Lung, Pancreas, Breast/Ovarian
140	799698			1	426			HCHAM08	Colon, Breast/Ovarian
141	800351	DNAJ homolog [Homo sapiens] >gi|1127833 heat shock protein hsp40 homolog [Homo sapiens] >pir|G02272|G02272 heat shock protein hsp40 homolog - human >sp|Q13431|Q13431 HEAT SHOCK PROTEIN HSP40 HOMOLOG. Length = 178	gi|1518918	282	860	83	84	HEMFP05	Pancreas, Breast/Ovarian

142	800573	26S protease subunit [Sus scrofa] >gi|3193258 (AF069053) proteasome subunit SUG1 [Bos taurus] >gnl|PID|d1012606 proteasomal ATPase (rat SUG1) [Rattus norvegicus] >gnl|PID|d1023806 (AB000491) proteasome p45/SUG [Rattus norvegicus] >gnl|PID|e199326 mSUG1 pr	gnl|PID|e235521	178	1383	93	93	HCEVS28	Lung, Breast/Ovarian
143	805815			15	1055			HCHAP80	Lung, Colon, Breast/Ovarian
144	806445			711	1028			HTELC67	Lung, Pancreas
145	810309	(AF098482) transcriptional coactivator p52 [Homo sapiens] >sp|G4050034|G4050034 TRANSCRIPTIONAL COACTIVATOR P52. Length = 333	gi|4050034	226	741	61	75	HNTDX22	Lung, Pancreas
146	811022			168	881			HISEA13	Lung, Pancreas
147	811023			13	234			HLWAW17	Lung, Pancreas, Colon, Breast/Ovarian
148	811143	cytokine inducible SH2-containing protein [Mus musculus] >pir|S55551|S55551 cytokine-inducible protein CIS - mouse >sp|Q62225|Q62225 CYTOKINE INDUCIBLE SH2-CONTAINING PROTEIN (SH2 DOMAIN CONTAINING PROTEIN INDUCED BY MULTIPLE CYTOKINES, SIC). Length = 257	gnl|PID|d1007285	3	887	90	92	HDQPA25	Lung, Breast/Ovarian
149	811381	FIN14 gene product [Mus musculus] >sp|Q61077|FI14_MOUSE FIBROBLAST GROWTH FACTOR INDUCIBLE PROTEIN 14 (FIN14). Length = 61	gi|1353711	1338	1511	86	91	HLYEK93	Colon, Breast/Ovarian

150	811595	CIRP [Homo sapiens] >gi|2924760 (AC004258) CIRP [Homo sapiens] >gi|2541973 (AF021336) DNA damage-inducible RNA binding protein [Homo sapiens] >sp|Q14011|Q14011 GLYCINE-RICH RNA BINDING PROTEIN CIRP. Length = 172	gn|PID|d1011874	1	609	100	100	HDTLA92	Pancreas, Breast/Ovarian
151	813000	Tera [Mus musculus] >sp|P70361|P70361 TERA. Length = 277	gi|1575505	95	850	84	86	HDPVZ64	Pancreas, Breast/Ovarian
152	813288	fau gene product [Homo sapiens] >gi|31305 fau 1 gene product [Homo sapiens] >pir|JC1278|JC1278 ubiquitin-like protein / ribosomal protein S30, cytosolic - human Length = 133	gi|31303	1	510	86	86	HCHMQ63	Lung, Breast/Ovarian
153	813431	DAP-1 [Homo sapiens] >pir|I37274|I37274 death-associated protein 1 - human >sp|P51397|DAP1_HUMAN DEATH-ASSOCIATED PROTEIN 1 (DAP-1). Length = 102	gi|434845	3	470	89	89	HWHQS70	Lung, Pancreas
154	813450	PISSLRE gene product [Homo sapiens] >pir|S49330|S49330 serine/threonine kinase (EC 2.7.1.-) pisslre - human >pir|I38116|I38116 gene PISSLRE protein - human >sp|Q15131|Q15131 PISSLRE MRNA. Length = 360	gi|556651	1	651	100	100	HCEEJ73	Lung, Pancreas
155	813478	retinoblastoma-binding protein mRbAp48 [Mus musculus] >pir|I49366|I49366 retinoblastoma-binding protein mRbAp48 - mouse Length = 461	gi|1016275	1	1398	99	100	HAJBH20	Lung, Pancreas, Breast/Ovarian
156	813505	ribosomal protein L23a [Homo sapiens] >gi|306549 homology to rat ribosomal protein L23 [Homo sapiens] {SUB 10-156} Length = 156	gi|404015	2	496	100	100	HDABR53	Lung, Pancreas

157	815552	(AJ011497) Claudin-9 [Homo sapiens] >sp|E1363658|E1363658 CLAUDIN-9. Length = 211	gnl|PID|e1363658	317	898	95	96	HUFEH29	Lung, Colon
158	815606	Ki-1/57 intracellular antigen [Homo sapiens] >sp|O75804|O75804 KI-1/57 INTRACELLULAR ANTIGEN (FRAGMENT). Length = 299	gi|3403154	218	1303	90	95	HDPRY63	Lung, Pancreas, Breast/Ovarian
159	816048	neutral protease alpha subunit [Homo sapiens] >gi|35328 protease small subunit (aa 1-268) [Homo sapiens] >gi|1905903 (AD001527) calcium-dependent protease, small (regulatory) subunit (calpain) (calcium-activated neutral proteinase) (CANP) [Homo sapiens] >	gi|179909	24	644	95	96	HTLCZ60	Lung, Breast/Ovarian
160	822978			94	156			HODEM46	Lung, Pancreas
161	823616			1449	1775			HCEME79	Pancreas, Colon
162	823981	(AF003130) similar to Achlya ambisexualis antheridiol steroid receptor (NID:g166306) [Caenorhabditis elegans] >sp|O01757|O01757 SIMILAR TO ACHLYA AMBISEXUALIS ANTHERIDIOL STEROID RECEPTOR. Length = 1043	gi|2088668	992	2617	60	78	HWHQH79	Lung, Breast/Ovarian
163	824364	drebrin E2 [Homo sapiens] >gnl|PID|d1005005 drebrin E [Homo sapiens] >pir|JN0809|JN0809 drebrin E (clone gDbh13) - human >sp|Q16643|DREB_HUMAN DREBRIN E. Length = 649	gi|392890	1	606	84	84	HCHPR34	Colon, Breast/Ovarian

164	824423	UDP-GalNAc:polypeptide N-acetylgalactosaminyl transferase [Homo sapiens] >pir|JC4223|JC4223 polypeptide N-acetylgalactosaminyltransferase (EC 2.4.1.41) - human >sp|Q10472|PAGT_HUMAN POLYPEPTIDE N-ACETYLGALACTOSAMINYLTRANSFERASE (EC 2.4.1.41) (PROTEIN- UDP	gi|971459	61	1743	100	100	HPWDL83	Lung. Pancreas
165	825279			36	602			116EDN61	Lung. Pancreas
166	825442			1	900			HTODA45	Colon. Breast/Ovarian
167	825548	ancient ubiquitous 46 kDa protein AUP46 precursor [Mus musculus] >sp|P70295|P70295 ANCIENT UBIQUITOUS PROTEIN PRECURSOR (AUP1). Length = 410	gi|1517822	473	1504	81	84	HLUDB77	Lung. Breast/Ovarian
168	825725	hNop56 [Homo sapiens] >sp|O00567|NO56_HUMAN NUCLEOLAR PROTEIN NOP56. Length = 602	gnl|PID|e1188703	25	723	99	99	HMWIV57	Lung. Pancreas
169	826639	H.sapiens mRNA for rat translocon-associated protein delta homolog [Homo sapiens] >gnl|PID|e212192 translocon-associated protein delta subunit precursor [Homo sapiens] >gnl|PID|e220312 translocon-associated protein delta subunit precursor [Homo sapiens] >	gi|1071681	1	561	100	100	HPTVX93	Lung. Colon. Breast/Ovarian
170	827079	(AL009171) 62D9.a [Drosophila melanogaster] >sp|E1198294|E1198294 62D9.A. Length = 1305	gnl|PID|e1198294	53	2176	71	85	HDAAD02	Lung. Breast/Ovarian

171	827153	pancreatitis-associated protein [Homo sapiens] >gi|312807 preprotein [Homo sapiens] >bbs|121222 PAP-H=pancreatitis-associated protein [human, pancreas, Peptide, 175 aa] [Homo sapiens] >gnl|PID|d1003233 PAP homologous protein [Homo sapiens] >pir|A49616|A49	gi|482909	54	602	90	90	HLQBS95	Pancreas, Colon, Breast/Ovarian
172	827351			1	639			HSKJE35	Colon, Breast/Ovarian
173	827503	(AC004003) serine/threonine kinase RICK; match to protein AF027706 (PID:g3123887) and mRNA AF027706 (NID:g3123886) [Homo sapiens] >gi|3290172 (AF064824) CARD-containing ICE associated kinase [Homo sapiens] >gi|3342910 (AF078530) receptor interacting prote	gi|3264574	255	1886	98	98	HLAAB36	Lung, Breast/Ovarian
174	827563	rhophilin [Mus musculus] >sp|Q61085|Q61085 GTP-RHO BINDING PROTEIN 1 (RHOPHILIN). Length = 643	gi|1176422	6	776	81	91	HBGDH11	Colon, Breast/Ovarian
175	827565	serine protease [Homo sapiens] Length = 492	gi|2507613	1	744	55	68	HCHAK72	Lung, Pancreas, Colon, Breast/Ovarian
176	827893	homology with GTP binding protein; putative [Caenorhabditis elegans] >pir|S44605|S44605 C02F5.3 protein - Caenorhabditis elegans Length = 573	gi|289610	165	836	62	75	HMSOT38	Lung, Pancreas
177	828072			1147	1305			HTECA53	Lung, Pancreas, Breast/Ovarian
178	828228			1105	1314			HWLAH78	Prostate, Colon

179	828241	cathepsin O [Homo sapiens] >pir|A55090|A55090 cathepsin O (EC 3.4.-.-) precursor - human >sp|P43234|CATO_HUMAN CATHEPSIN O PRECURSOR (EC 3.4.22.-). Length = 321	gi|574804	2	1012	93	93	HWBBP30	Lung, Pancreas, Prostate
180	828287	histone (H2A.Z) [Bos taurus] >gi|410 histone H2A.Z (AA 1-127) [Bos taurus] >gi|184060 histone (H2A.Z) [Homo sapiens] >gi|31975 histone H2A.Z (AA 1-127) [Homo sapiens] >gi|3649600 histone [Homo sapiens] >gi|204599 histone (H2A.Z) [Rattus norvegicus] >gi|57	gi|163150	171	572	100	100	HUSIS02	Lung, Pancreas, Prostate, Breast/Ovarian
181	828364			663	1340			HWHGT17	Pancreas, Breast/Ovarian
182	828371	complement component C1s [Homo sapiens] >gi|179648 complement subcomponent C1s precursor [Homo sapiens] >gi|763110 complement protein C1s precursor [Homo sapiens] >pir|A40496|C1HUS complement subcomponent C1s (EC 3.4.21.42) precursor - human >sp|P09871|C1	gi|179646	4	2283	97	97	HLQCQ12	Lung, Pancreas, Colon, Breast/Ovarian
183	828403	DNA-binding protein [Homo sapiens] >pir|A44478|A44478 probable cell growth or differentiation regulator (alternatively spliced type I transcript) - human >sp|Q02833|Q02833 PUTATIVE TRANSCRIPTIONAL REGULATORY PROTEIN HRC1. Length = 373	gi|184390	1	648	98	98	HDTHL82	Lung, Pancreas, Colon
184	828501	(AF056302) eIF-2alpha kinase [Drosophila melanogaster] >sp|O61651|O61651 EIF-2ALPHA KINASE. Length = 1589	gi|3046551	1	1812	36	58	HBMDG73	Lung, Colon, Breast/Ovarian

185	828520	(AJ010840) ATP-dependent RNA helicase [Homo sapiens] >sp|E1321519|E1321519 ATP-DEPENDENT RNA HELICASE (FRAGMENT). Length = 420	gnl|PID|e1321519	445	1821	91	91	HRGBN47	Prostate, Breast/Ovarian
186	828527			723	926			HSKGQ05	Lung, Pancreas. Prostate, Breast/Ovarian
187	828538			332	976			HPWDF55	Lung, Prostate, Breast/Ovarian
188	828541	pre-pump-1 proteinase (AA -17 to 250) [Homo sapiens] >gi|35803 PUMP [Homo sapiens] >pir|B28816|KCHUM matrilysin (EC 3.4.24.23) precursor - human >sp|P09237|COG7_HUMAN MATRILYSIN PRECURSOR (EC 3.4.24.23) (PUMP-1 PROTEASE) (UTERINE METALLOPROTEINASE) (MATRI	gi|35799	43	933	100	100	HRACJ32	Pancreas, Prostate, Colon
189	828549	thrombospondin 2 [Homo sapiens] >pir|A47379|TSHUP2 thrombospondin 2 precursor - human Length = 1172	gi|307506	26	1738	94	94	HFIAL22	Pancreas, Colon
190	828562			1	342			HPWBR24	Pancreas, Prostate
191	828576			3	731			HPTVU91	Pancreas, Prostate, Colon
192	828602			1050	1568			HPRAT58	Lung, Prostate
193	828628	tumor-associated antigen [Homo sapiens] >pir|A36056|A36056 tumor-associated antigen CO-029 - human >sp|P19075|CO02_HUMAN TUMOR-ASSOCIATED ANTIGEN CO-029. Length = 237	gi|180926	307	1029	94	94	HPRCM33	Pancreas, Prostate, Colon

194	828667	cytochrome c-1 [Homo sapiens] >sp|P08574|CY1_HUMAN CYTOCHROME C1. HEME PROTEIN PRECURSOR. >gi|181238 cytochrome c1 [Homo sapiens] {SUB 99-325} Length = 325	gi|181240	2	1006	85	85	HKAOB02	Pancreas. Breast/Ovarian
195	828684	p55CDC [Homo sapiens] >pir|A56021|A56021 probable cell division control protein p55CDC - human >sp|Q12834|Q12834 P55CDC. Length = 499	gi|468032	41	1573	92	92	HPJAE35	Pancreas. Prostate
196	828727	(AF044954) NADH:ubiquinone oxidoreductase PDSW subunit [Homo sapiens] >gi|4165091 (AF088991) NADH-ubiquinone oxidoreductase PDSW subunit [Homo sapiens] Length = 172	gi|4164442	3	629	93	93	HMCBB12	Lung. Prostate. Breast/Ovarian
197	828734	homologue of Drosophila Fat protein [Homo sapiens] >sp|Q14517|Q14517 CADHERIN-RELATED TUMOR SUPPRESSOR HOMOLOG PRECURSOR (FAT PROTEIN HOMOLOG). >gnl|PID|d1022418 cadherin [Homo sapiens] {SUB 993-1132} Length = 4590	gi|1107687	1	657	99	99	HSRAB84	Pancreas. Colon. Breast/Ovarian
198	828750	(AF035940) similar to mago nashi [Homo sapiens] >gi|2330011 (AF007862) mm-Mago [Mus musculus] >gi|2909828 (AF035939) similar to mago nashi [Mus musculus] >sp|O35169|O35169 MM-MAGO. >sp|G2909830|G2909830 MAGOH. >sp|P50606|MGN_HUMAN MAGO NASHI PROTEIN HOMOL	gi|2909830	13	546	100	100	HPIAC11	Pancreas. Prostate. Breast/Ovarian

199	828842	(AB007191) AMY-1 [Homo sapiens] >gnl|PID|d1009980 c-myc binding protein [Homo sapiens] >sp|Q99417|Q99417 C-MYC BINDING PROTEIN. Length = 103	gnl|PID|d1023271	1	363	98	100	HOUGA12	Pancreas. Prostate. Breast/Ovarian
200	828843	p48 [Homo sapiens] >sp|P50502|HIP_HUMAN HSC70-INTERACTING PROTEIN (PROGESTERONE RECEPTOR-ASSOCIATED P48 PROTEIN). >gi|1857033 SCN6 gene product [Homo sapiens] {SUB 99-369} Length = 369	gi|904032	3	761	99	100	HOVBK85	Lung, Pancreas. Prostate
201	828851	(AF054284) spliceosomal protein SAP 155 [Homo sapiens] >sp|G4033735|G4033735 SPLICEOSOMAL PROTEIN SAP 155. >gi|3387899 (AF070540) putative nuclear protein [Homo sapiens] {SUB 1011-1304} Length = 1304	gi|4033735	1	1029	98	98	HOSGA73	Pancreas. Prostate
202	828856	thymidine kinase (EC 2.7.1.21) [Homo sapiens] >gi|339719 thymidine kinase [Homo sapiens] >pir|A27318|KIHUT thymidine kinase (EC 2.7.1.21), cytosolic - human >sp|P04183|KITH_HUMAN THYMIDINE KINASE, CYTOSOLIC (EC 2.7.1.21). >gi|339713 thymidine kinase [Homo	gi|339709	1	804	99	100	HOHEN75	Prostate. Breast/Ovarian
203	828862	tyrosine kinase receptor [Homo sapiens] >pir|B41527|B41527 transforming protein (axl(-)) - human Length = 885	gi|292870	1	417	98	98	HOHBI90	Prostate. Breast/Ovarian
204	828870	TRAM protein [Homo sapiens] >pir|S30034|S30034 translocating chain-associating membrane protein - human >sp|Q15629|Q15629 TRAM PROTEIN. Length = 374	gi|37265	32	1279	94	94	HOEKU65	Lung, Pancreas. Colon

205	828873	precursor polypeptide (AA -31 to 1139) [Homo sapiens] >gi|538354 thrombospondin [Homo sapiens] {SUB 1-397} >gi|339669 thrombospondin [Homo sapiens] {SUB 1028-1170} >gi|532689 thrombospondin-1p180 [Homo sapiens] {SUB 364-422} Length = 1170	gi|37465	1	1398	100	100	HOHCJ26	Lung, Pancreas, Prostate, Colon, Breast/Ovarian
206	828892	keratin [Homo sapiens] >sp|Q14533|Q14533 KERATIN (HAIR TYPE II BASIC KERATIN) (KERATIN LIKE). >gnl|PID|e118093 hair type II basic keratin [Homo sapiens] {SUB 81-505} >gi|951272 keratin like [Homo sapiens] {SUB 249-505} >bbs|161491 type II hair keratin {cl	gnl|PID|e321549	3	653	90	91	HOGAA83	Lung, Prostate, Breast/Ovarian
207	828893	ESX [Homo sapiens] >gi|1841523 ESE-1b [Homo sapiens] >gi|2338756 (AF017307) Ets-related transcription factor [Homo sapiens] >gi|2384740 (AF016295) Ets transcription factor [Homo sapiens] >gi|2459797 epthelial-specific ets protein [Homo sapiens] >sp|P78545	gi|1754538	36	1253	86	86	HOGAS09	Pancreas, Prostate, Colon, Breast/Ovarian
208	828897	prostasin [Homo sapiens] >gi|862305 prostasin [Homo sapiens] >pir|A57014|A57014 prostasin (EC 3.4.21.-) precursor - human >sp|G565130|G565130 PROSTASIN=SERINE PROTEINASE {N-TERMINAL}. {SUB 45-64} Length = 343	gi|1143194	59	811	92	92	HBCAY53	Pancreas, Colon, Breast/Ovarian

209	828910	light chain 3 subunit of microtubule-associated proteins 1A and 1B [Rattus norvegicus] >pir|A53624|A53624 microtubule-associated protein 1 light chain 3 - rat >sp|Q62625|MPL3_RAT MICROTUBULE-ASSOCIATED PROTEINS 1A/1B LIGHT CHAIN 3 (MAP1A/MAP1B LC3). {SUB	gi|455109	28	540	96	98	HOHDY41	Prostate, Colon
210	828927	cytochrome c oxidase subunit Va [Homo sapiens] >pir|JT0342|OTHU5A cytochrome-c oxidase (EC 1.9.3.1) chain Va precursor - human >sp|P20674|COXA_HUMAN CYTOCHROME C OXIDASE POLYPEPTIDE VA PRECURSOR (EC 1.9.3.1). >gi|3859864 (AF067635) cytochrome c oxidase su	gi|695360	1	567	99	99	HHFJM88	Lung, Breast/Ovarian
211	828932	80K-H protein [Homo sapiens] >gi|1293640 protein kinase C substrate 80K-H [Homo sapiens] >pir|A32469|A32469 80K protein H precursor - human >sp|P14314|G19P_HUMAN PROTEIN KINASE C SUBSTRATE, 80 KD PROTEIN, HEAVY CHAIN (PKCSH) (80K-H PROTEIN). Length = 527	gi|182855	82	1026	83	83	HNTAC57	Lung, Pancreas, Prostate, Breast/Ovarian
212	828933	Csa-19 [Homo sapiens] Length = 217	gi|531171	439	852	97	98	HEMCA07	Lung, Pancreas, Breast/Ovarian
213	828941	ORF YJL115w [Saccharomyces cerevisiae] >gi|171091 ASF1 [Saccharomyces cerevisiae] >pir|S30766|S30766 ASF1 protein - yeast (Saccharomyces cerevisiae) >sp|P32447|ASF1_YEAST ANTI-SILENCING PROTEIN 1. Length = 279	gi|1008304	1	729	59	74	HMGBJ25	Lung, Pancreas, Colon, Breast/Ovarian

214	828957	F31C3.5 [Caenorhabditis elegans] >sp|O62193|O62193 F31C3.5 PROTEIN. Length = 180	gnl|PID|e1346411	3	635	37	68	HMWHG54	Prostate, Breast/Ovarian
215	828963	house-keeping protein [Mus musculus] >pir|S27870|S27870 house-keeping protein - mouse >sp|Q61669|Q61669 HOUSE-KEEPING PROTEIN 1. Length = 396	gi|193871	73	1293	55	77	HMWBH91	Lung, Prostate, Colon, Breast/Ovarian
216	828964			639	905			HMWFZ60	Pancreas, Prostate, Colon, Breast/Ovarian
217	828966	S-adenosylhomocysteine hydrolase [Homo sapiens] >pir|A43629|A43629 adenosylhomocysteinase (EC 3.3.1.1) - human Length = 432	gi|178279	2	1372	98	98	HMWFV54	Lung, Pancreas, Prostate, Breast/Ovarian
218	828967	putative tRNA synthetase-like protein [Homo sapiens] >gi|4104935 (AF042347) putative phenylalanyl-tRNA synthetase alpha-subunit; PheHA [Homo sapiens] >sp|E317305|E317305 PUTATIVE TRNA SYNTHETASE-LIKE PROTEIN. >sp|G2102679|G2102679 PUTATIVE TRNA SYNTHETASE	gi|2102679	3	1535	98	98	HMUBT12	Pancreas, Prostate, Breast/Ovarian
219	828977	insulin-like growth factor binding protein 2 [Homo sapiens] >bbs|106618 insulin-like growth factor binding protein-2, IGFBP-2 [human, placenta, Peptide, 328 aa] [Homo sapiens] >pir|A41927|A41927 insulin-like growth factor-binding protein 2 precursor - hum	gi|179477	2	685	100	100	HMVAW27	Lung, Pancreas, Prostate, Breast/Ovarian

220	828978	annexin IV (placental anticoagulant protein II) [Homo sapiens] >gnl|PID|d1011889 annexin IV (carbohydrtate-binding protein p33/41) [Homo sapiens] >pir|A42077|A42077 annexin IV - human >sp|P09525|ANX4_HUMAN ANNEXIN IV (LIPOCORTIN IV) (ENDONEXIN I) (CHROMOB	gi|178699	213	1184	100	100	HNTMH78	Lung, Pancreas, Prostate
221	828979			16	1080			HMUBO53	Lung, Pancreas, Prostate, Colon, Breast/Ovarian
222	829001			1621	1959			HMSJR30	Lung, Pancreas, Prostate, Breast/Ovarian
223	829003	plasma gelsolin [Homo sapiens] >pir|A03011|FAHUP gelsolin precursor, plasma - human >sp|P06396|GELS_HUMAN GELSOLIN PRECURSOR, PLASMA (ACTIN-DEPOLYMERIZING FACTOR) (ADF) (BREVIN) (AGEL). >gnl|PID|e20565 plasma gelsolin (AA 49-117) [Homo sapiens] {SUB 49-11	gi|736249	635	2536	99	99	HMSKA53	Lung, Pancreas, Prostate
224	829016	(AB006625) The human homolog of a mouse imprinted gene, Peg3. [Homo sapiens] >sp|P78418|P78418 KIAA0287 (PEG3) (FRAGMENT). >gi|1899244 PEG3 [Homo sapiens] {SUB 518-1132} Length = 1132	dbj|AB006625_1	409	759	87	87	HMIAI73	Prostate, Breast/Ovarian
225	829027	ras-like protein [Homo sapiens] >pir|D34788|TVHUC4 transforming protein ras (teratocarcinoma clone TC10) - human Length = 213	gi|190881	2	577	100	100	HMIBE59	Prostate, Colon

226	829028	RnudC gene product [Rattus norvegicus] >pir|A55897|A55897 prolactin-induced T cell protein c15 - rat >sp|Q63525|Q63525 C15 MRNA. Length = 332	gi|619907	31	1110	95	98	HMGBQ56	Pancreas, Prostate, Breast/Ovarian
227	829031	protocadherin X [Mus musculus] >sp|G4099553|G4099553 PROTOCADHERIN X. Length = 928	gi|4099553	116	637	90	93	HMGB169	Lung, Pancreas, Prostate, Breast/Ovarian
228	829034			28	1362			HMEIY69	Pancreas, Prostate
229	829036	Similar to B.subtilis Poly(A) polymerase (SW:PAPS_BACSU) [Caenorhabditis elegans] >sp|Q93795|Q93795 F55B12.4 PROTEIN. Length = 440	gnl|PID|e1347205	114	1151	67	81	HMELJ75	Pancreas, Prostate
230	829049	UDP-Gal:GlcNAc galactosyltransferase [Homo sapiens] >sp|O60910|O60910 UDP-GAL:GLCNAC GALACTOSYLTRANSFERASE. Length = 393	gnl|PID|e1283714	233	1444	94	94	HMEFQ33	Prostate, Colon
231	829073			193	843			HLYCD85	Pancreas, Prostate
232	829075			2	484			HMAAD66	Lung, Pancreas, Prostate, Breast/Ovarian
233	829076			3	665			HADDC41	Lung, Pancreas, Breast/Ovarian
234	829080			3	500			HMABG80	Prostate, Breast/Ovarian
235	829087	small GTP-binding protein [Oryctolagus cuniculus] >pir|A48500|A48500 small GTP-binding protein Rab25 - rabbit Length = 213	gi|436001	157	873	95	97	HLWBY67	Pancreas, Prostate, Breast/Ovarian

236	829092	UDP-galactose translocator [Homo sapiens] >pir|JC4903|JC4903 UDP-galactose transporter, splice form 1 - human Length = 393	gnl|PID|d1013353	1	513	85	85	HLWBC74	Pancreas, Prostate
237	829095			3	425			HLWBM89	Lung, Pancreas, Prostate, Colon, Breast/Ovarian
238	829096	antiquitin=26g turgor protein homolog [human, kidney, Peptide, 511 aa] [Homo sapiens] >pir|A54676|A54676 antiquitin - human >sp|P49419|DHAX_HUMAN ANTIQUITIN (EC 1.2.1.-). Length = 511	bbs|158840	552	1628	97	97	HLWAO28	Prostate, Breast/Ovarian
239	829118	nuclear autoantigen fo 14 kDa [Homo sapiens] >sp|O43805|O43805 NUCLEAR AUTOANTIGEN FO 14 KDA. Length = 119	gnl|PID|e322419	2	415	99	99	HLSDA35	Lung, Prostate
240	829152	unknown protein precursor [Homo sapiens] >pir|JN0596|JN0596 fibrinogen-related protein HFREP-1 precursor - human >sp|Q08830|Q08830 FIBRINOGEN-LIKE PROTEIN 1 PRECURSOR. Length = 312	gnl|PID|d1003846	215	1231	95	95	HLICU82	Lung, Pancreas, Prostate
241	829160	ubiquitin-conjugating enzyme UbcH6 [Homo sapiens] Length = 193	gi|1064914	2	769	83	83	HLFBF56	Lung, Pancreas, Prostate, Colon
242	829163			403	930			HSPBG80	Lung, Pancreas, Breast/Ovarian
243	829176	C4b-binding protein alpha chain [Homo sapiens] >gi|190502 C4b-binding protein alpha chain [Homo sapiens] >pir|A33568|NBHUC4 C4b-binding protein alpha chain precursor - human >sp|P04003|C4BP_HUMAN C4B-BINDING PROTEIN ALPHA CHAIN PRECURSOR (PROLINE-RICH PRO	gi|190500	3	662	100	100	HLQBR92	Lung, Pancreas
244	829204			515	913			HL1SB22	Prostate, Breast/Ovarian

245	829207			111	977			HL1SA66	Prostate, Breast/Ovarian
246	829228			1	2508			HKGBQ77	Lung, Prostate, Colon
247	829252			96	1322			HKAPI21	Pancreas, Prostate
248	829254			1	483			HKFBI96	Lung, Pancreas, Prostate, Breast/Ovarian
249	829269			121	474			HKAEE96	Lung, Pancreas, Prostate, Colon, Breast/Ovarian
250	829277			3	596			HJPCG91	Lung, Prostate
251	829290			100	207			HJBDL52	Lung, Pancreas, Prostate, Breast/Ovarian
252	829294			3	1847			HISDU47	Pancreas, Prostate
253	829299			3	794			HISEC32	Lung, Pancreas, Prostate
254	829308	dJ14O9.2 (Melanoma-Associated Antigen MAGE LIKE) [Homo sapiens] >sp|O76058|O76058 DJ14O9.2 (MELANOMA-ASSOCIATED ANTIGEN MAGE LIKE). Length = 606	gnl|PID|e1311294	207	938	47	70	HIBCN93	Lung, Pancreas, Prostate, Colon, Breast/Ovarian
255	829349	ribosomal protein S15a [Rattus norvegicus] >pir|JC2234|JC2234 ribosomal protein S15a - rat Length = 130	gi|495273	152	547	100	100	HICAF44	Lung, Pancreas, Prostate, Breast/Ovarian
256	829354	RAD4 gene product [Saccharomyces cerevisiae] Length = 730	gi|4271	1	1113	44	65	HAJBD51	Lung, Pancreas, Breast/Ovarian

257	829388	DNase protein [Homo sapiens] >gi|1620214 XIB [Homo sapiens] >pir|JC4633|JC4633 DNase I-like endonuclease (EC 3.1.-.-) - human >sp|P49184|DRNL_HUMAN MUSCLE-SPECIFIC DNASE I-LIKE PRECURSOR (EC 3.1.21.-) (DNASE X) (XIB). Length = 302	gi|929628	319	1281	94	94	HUVCJ22	Lung, Pancreas, Colon, Breast/Ovarian
258	829540			258	437			HAPOU28	Lung, Pancreas, Colon, Breast/Ovarian
259	829626	mannosyl-oligosaccharide 1,2-alpha-mannosidase (EC 3.2.1.113) - rabbit (fragment) >gi|474282 mannosyl-oligosaccharide alpha-1,2-mannosidase [Oryctolagus cuniculus] {SUB 12-480} Length = 480	pir|B54408|B54408	3	764	75	88	HCEES14	Lung, Pancreas, Colon, Breast/Ovarian
260	829730	underexpressed in thyroid tissue after TSH stimulation [Canis familiaris] >sp|Q28283|Q28283 C5FW PROTEIN. Length = 343	gnl|PID|e252512	455	1153	62	75	HAJBK53	Pancreas, Breast/Ovarian
261	829892	(AF053651) cellular apoptosis susceptibility protein [Homo sapiens] >sp|O75432|O75432 CELLULAR APOPTOSIS SUSCEPTIBILITY PROTEIN. Length = 971	gi|3598795	64	1053	85	85	HAMFJ43	Lung, Prostate
262	829933	(AF035606) calcium binding protein [Homo sapiens] >sp|O75340|O75340 CALCIUM BINDING PROTEIN. Length = 191	gi|3342794	1	540	86	86	HAICT76	Pancreas, Prostate
263	829938	(AF067855) geminin [Homo sapiens] >sp|O75496|O75496 GEMININ. Length = 209	gi|3249005	230	952	93	93	HAIBS55	Pancreas, Prostate
264	829969			551	814			HACCB64	Lung, Pancreas, Prostate, Breast/Ovarian

265	829982	(AF020352) NADH:ubiquinone oxidoreductase 15 kDa IP subunit [Homo sapiens] >gi|2911482 (AF047434) NADH-ubiquinone oxidoreductase 15kDa subunit; CI-15 protein [Homo sapiens] >sp|O43920|NIPM_HUMAN NADH-UBIQUINONE OXIDOREDUCTASE 15 KD SUBUNIT (EC 1.6.5.3) (E	gi|2655055	28	399	100	100	HABGE25	Prostate, Breast/Ovarian
266	830007	catechol-O-methyltransferase [Homo sapiens] >gi|403304 catechol O-methyltransferase [Homo sapiens] >pir|S37406|A38459 catechol O-methyltransferase (EC 2.1.1.6) - human >sp|P21964|COMT_HUMAN CATECHOL O-METHYLTRANSFERASE, MEMBRANE-BOUND FORM (EC 2.1.1.6) (M	gi|180920	110	1006	99	99	H6EDW66	Lung, Prostate, Breast/Ovarian
267	830019	(AF030249) putative dienoyl-CoA isomerase [Homo sapiens] >gi|564065 peroxisomal enoyl-CoA hydratase-like protein [Homo sapiens] >pir|I38882|I38882 peroxisomal enoyl-CoA hydratase-like protein - human >sp|Q13011|ECH1_HUMAN PROBABLE PEROXISOMAL ENOYL-COA HY	gi|2623168	77	976	94	96	H2MAC92	Prostate, Breast/Ovarian
268	830073			1	690			HBWBK27	Lung, Pancreas, Breast/Ovarian
269	830130			1	177			H2LAD55	Lung, Prostate, Breast/Ovarian
270	830134			16	1290			H2CBP53	Lung, Pancreas, Prostate, Colon, Breast/Ovarian

271	830135	neutrophil gelatinase associated lipocalin [Homo sapiens] >sp|P80188|NGAL_HUMAN NEUTROPHIL GELATINASE-ASSOCIATED LIPOCALIN PRECURSOR (NGAL) (P25) (25 KD ALPHA-2-MICROGLOBULIN-RELATED SUBUNIT OF MMP-9) (LIPOCALIN-2) (ONCOGENE 24P3). Length = 198	gi|929657	2	763	100	100	H2MAC06	Pancreas, Prostate, Breast/Ovarian
272	830148	snRNP polypeptide B [Homo sapiens] >sp|Q15182|Q15182 SNRNP POLYPEPTIDE B. Length = 285	gi|190247	96	839	79	79	HAICK77	Lung, Prostate, Breast/Ovarian
273	830149	threonyl-tRNA synthetase [Homo sapiens] >pir|A38867|YSHUT threonine--tRNA ligase (EC 6.1.1.3) - human Length = 712	gi|1464742	3	2333	95	95	H2CBC04	Lung, Pancreas, Prostate
274	830154	spectrin SH3 domain binding protein 1 [Homo sapiens] >sp|O76049|O76049 SPECTRIN SH3 DOMAIN BINDING PROTEIN 1. Length = 508	gi|3165429	2	1081	100	100	HYAAC49	Lung, Pancreas
275	830183			92	358			HWLQF08	Pancreas, Breast/Ovarian
276	830194	heat shock protein 84 - mouse >pir|B34461|B34461 heat shock protein 90 beta - rabbit (fragment) {SUB 1-25} >sp|P30947|HS9B_RABIT HEAT SHOCK PROTEIN HSP 90-BETA (HSP 84) (FRAGMENT). {SUB 2-25} >pir|S13268|S13268 heat shock protein, 90K - bovine (fragment)	pir|A35569|HHMS84	3	1043	100	100	HLDCP20	Lung, Pancreas, Breast/Ovarian
277	830207	(AF016437) contains similarity to a C2H2-type zinc finger [Caenorhabditis elegans] >sp|O16350|O16350 F13H6.1 PROTEIN. Length = 631	gi|2315332	173	1051	45	63	HWLMF07	Pancreas, Colon
278	830242			85	654			HWLUF58	Lung, Pancreas

279	830328	putative cyclin G1 interacting protein [Homo sapiens] >sp|O43257|O43257 PUTATIVE CYCLIN G1 INTERACTING PROTEIN. Length = 154	gi|2668505	304	954	81	81	HWLEL26	Lung, Colon, Breast/Ovarian
280	830340	putative cell surface antigen [Rattus norvegicus] >sp|P97881|P97881 PUTATIVE CELL SURFACE ANTIGEN. Length = 547	gi|1890275	1	336	63	81	HWLEG68	Pancreas, Colon
281	830341	peroxisomal acyl-coenzyme A oxidase, AOX [human, liver, Peptide, 661 aa] [Homo sapiens] Length = 661	bbs|144907	1	648	100	100	HSIA1179	Lung, Pancreas
282	830351			3	656			HWHQT21	Colon, Breast/Ovarian
283	830358			456	716			HSUAE53	Lung, Colon, Breast/Ovarian
284	830390	platelet membrane glycoprotein IIIa beta subunit [Homo sapiens] >sp|O15495|O15495 PLATELET MEMBRANE GLYCOPROTEIN IIIA BETA SUBUNIT. Length = 784	gi|2443452	2	523	90	90	HWGQA69	Pancreas, Colon
285	830400	phosphate carrier protein [Homo sapiens] >pir|B53737|B53737 phosphate carrier protein, form B - human Length = 361	gi|38262	2	1078	99	100	HWHPY68	Lung, Pancreas, Breast/Ovarian
286	830437	IgG Fc receptor I [Homo sapiens] >gi|292169 Fc gamma receptor I [Homo sapiens] >pir|A39878|A39878 Fc gamma (IgG) receptor I-A (high affinity) precursor - human >sp|Q92663|Q92663 FC GAMMA RECEPTOR I. Length = 374	gi|180279	3	1199	91	91	HWABG32	Lung, Colon

287	830458	HBp15/L22 [Sus scrofa] >gnl|PID|d1005074 HBp15/L22 [Mus musculus] >pir|JC2121|JC2121 heparin-binding protein 15 - pig >pir|JC2119|JC2119 heparin-binding protein 15 - mouse Length = 128	gnl|PID|d1005075	1	441	70	70	HDQMF96	Lung, Pancreas
288	830466			988	1260			HOEEZ61	Lung, Colon
289	830497	tenascin X [Homo sapiens] >sp|P78530|P78530 TENASCIN X (TENASCIN-X). >gi|2347137 (AF019413) tenascin X [Homo sapiens] {SUB 2593-4289} >pir|A42175|A42175 tenascin homolog 3.9kF3-3 - human (fragment) {SUB 2793-2880} >pir|B42175|B42175 tenascin homolog 3.9kF	gi|1841546	2	1531	99	99	HUFBX52	Lung, Breast/Ovarian
290	830511	carcinoembryonic antigen [Homo sapiens] >gi|178677 carcinoembryonic antigen precursor [Homo sapiens] >pir|A36319|A36319 carcinoembryonic antigen precursor - human >sp|P06731|CCEM_HUMAN CARCINOEMBRYONIC ANTIGEN PRECURSOR (CEA) (MECONIUM ANTIGEN 100) (CD66E	gi|180223	3	1292	99	99	HWLGV67	Pancreas, Colon
291	830512	carcinoembryonic antigen [Homo sapiens] >gi|178677 carcinoembryonic antigen precursor [Homo sapiens] >pir|A36319|A36319 carcinoembryonic antigen precursor - human >sp|P06731|CCEM_HUMAN CARCINOEMBRYONIC ANTIGEN PRECURSOR (CEA) (MECONIUM ANTIGEN 100) (CD66E	gi|180223	3	2213	87	89	HUFCI29	Lung, Pancreas

292	830513			3	215			HPRTG72	Lung, Colon, Breast/Ovarian
293	830540	protein kinase MUK2 [Rattus norvegicus] >gi|2772514 serine/threonine protein kinase [Rattus norvegicus] >sp|P35465|PAK1_RAT SERINE/THREONINE-PROTEIN KINASE PAK-ALPHA (EC 2.7.1.-) (P68-PAK) (P21-ACTIVATED KINASE) (ALPHA-PAK) (PROTEIN KINASE MUK2). Length	gi|1399508	2	733	100	100	HTLHR67	Lung, Pancreas, Colon
294	830550	guanine nucleotide-binding regulatory protein-beta-2 subunit [Homo sapiens] >gi|339935 transducin beta-2 subunit [Homo sapiens] >gi|3135310 (AF053356) GNB2 [Homo sapiens] >pir|B26617|RGHUB2 GTP-binding regulatory protein beta-2 chain - human >sp|P11016|GB	gi|386751	3	500	100	100	HTWJC08	Lung, Breast/Ovarian
295	830567			141	377			HTTBH33	Lung, Pancreas
296	830586	(2'-5')oligoadenylate synthetase [Homo sapiens] Length = 364	gnl|PID|d1000487	2	1192	98	98	HKACP86	Pancreas, Prostate, Breast/Ovarian
297	830632	P2 gene for c subunit of mitochondrial ATP synthase gene product [Homo sapiens] >gnl|PID|d1002921 ATP synthase subunit c precursor [Homo sapiens] >pir|S34067|S34067 H+-transporting ATP synthase (EC 3.6.1.34) lipid-binding protein P2 precursor, mitochondri	gi|38432	264	803	85	85	HTPCV95	Lung, Breast/Ovarian

298	830645	propionyl CoA carboxylase beta subunit, beta PCC {EC 6.4.1.3} [human, liver, placenta, HL 1008, Peptide, 539 aa] [Homo sapiens] >pir|A53020|A53020 propionyl-CoA carboxylase (EC 6.4.1.3) beta chain precursor - human >gi|3036995 propionyl-CoA carboxylase B	bbs|140816	54	1505	99	99	HTEDS58	Lung, Pancreas, Colon
299	830652	strong homology to human RING3 sequence [Homo sapiens] >sp|O60885|O60885 HUNKI MRNA. Length = 722	gnl|PID|e1290115	1	177	64	64	HUKFL74	Lung, Colon
300	830659	CDC42 GTP-binding protein [Canis familiaris] >gi|183490 GTP-binding protein G25K [Homo sapiens] >gi|293321 CDC42Mm [Mus musculus] >gi|1049309 CDC42 protein [Mus musculus] >pir|A39265|A39265 GTP-binding protein G25K, placental - human >pir|S57563|S57563 CD	gi|887408	118	714	100	100	HKAOE74	Lung, Pancreas, Breast/Ovarian
301	830696			2	514			HSTBJ95	Lung, Breast/Ovarian
302	830706			2457	2909			HELFG05	Pancreas, Breast/Ovarian
303	830743	ATP SYNTHASE EPSILON CHAIN, MITOCHONDRIAL (EC 3.6.1.34). Length = 50	sp|P56381|ATPE_HUMAN	53	262	100	100	HCBBA51	Lung, Colon
304	830770	p21-activated protein kinase [Homo sapiens] >pir|S58682|S58682 protein kinase, p21-activated (EC 2.7.1.-) - human Length = 525	gi|780808	1	498	99	99	HEMCG27	Lung, Colon, Breast/Ovarian
305	830830	(AF002822) cyclin B2 [Homo sapiens] >sp|G4101270|G4101270 CYCLIN B2. Length = 398	gi|4101270	99	1358	99	99	HROCE57	Lung, Pancreas, Colon

306	830838			1	747			HS2AF59	Lung, Pancreas, Colon, Breast/Ovarian
307	830851			2	718			HTXLJ25	Pancreas, Colon
308	830853			2	1183			HRDDS42	Pancreas, Colon
309	830856			542	874			HSAAX81	Colon, Breast/Ovarian
310	830862	ribosomal protein [Homo sapiens] >gi|453281 ribosomal protein S23 [Rattus norvegicus] >pir|S41955|S41955 ribosomal protein S23, cytosolic - rat >pir|S42105|S42105 ribosomal protein S23, cytosolic - human >pir|I52292|I52292 ribosomal protein S23 - rat >gnl	gnl|PID|d1003910	3	518	100	100	HLCC05	Lung, Prostate, Breast/Ovarian
311	830879	(AJ002120) Zfx [Monodelphis domestica] >sp|O19019|O19019 ZFX TYPE GENE (FRAGMENT). Length = 180	gnl|PID|e354749	2	592	39	58	HVAAB82	Pancreas, Colon
312	830919			69	536			HOUHK65	Pancreas, Breast/Ovarian
313	830969	(AF005046) serine/threonine kinase [Homo sapiens] >gnl|PID|e1371371 (AJ011855) PAK4 protein [Homo sapiens] >sp|G4101587|G4101587 SERINE/THREONINE KINASE. Length = 591	gi|4101587	140	514	96	96	HOGAU20	Pancreas, Breast/Ovarian
314	830991	insulin-like growth factor-binding protein [Homo sapiens] >gi|386791 growth factor-binding protein-3 [Homo sapiens] >gi|398164 insulin-like growth factor binding protein 3 [Homo sapiens] >pir|A36578|IOHU3 insulin-like growth factor-binding protein 3 precu	gi|183116	2	607	86	86	HDLAE73	Pancreas, Breast/Ovarian

315	831002	cyclin [Homo sapiens] >gi|387005 proliferating cell nuclear antigen (PCNA) [Homo sapiens] >pir|A27445|WMHUET proliferating cell nuclear antigen - human >sp|P12004|PCNA_HUMAN PROLIFERATING CELL NUCLEAR ANTIGEN (PCNA) (CYCLIN). Length = 261	gi|181272	168	974	100	100	HOEMJ36	Colon, Breast/Ovarian
316	831003	T-plastin - human >sp|P13797|PLST_HUMAN T-PLASTIN. {SUB 4-630} >gi|190028 T-plastin . polypeptide [Homo sapiens] {SUB 61-630} >gi|339848 T-plastin [Homo sapiens] {SUB 1-143} >gi|292832 T-plastin [Homo sapiens] {SUB 588-630} Length = 630	pir|A34789|A34789	91	2007	94	95	HAIBD64	Lung, Pancreas
317	831021			474	662			HE8BN45	Pancreas, Colon, Breast/Ovarian
318	831036	(AJ006068) dTDP-D-glucose 4,6-dehydratase [Homo sapiens] >sp|E1363774|E1363774 DTDP-D-GLUCOSE 4,6-DEHYDRATASE (EC 4.2.1.46). Length = 350	gnl|PID|e1363774	1	621	100	100	HNTSQ61	Pancreas, Colon
319	831071	lrp gene product [Homo sapiens] >pir|S57723|S57723 lrp protein - human >sp|Q14764|MVP_HUMAN MAJOR VAULT PROTEIN (MVP) (LUNG RESISTANCE-RELATED PROTEIN). Length = 896	gi|895840	67	2610	94	94	HWLEG93	Lung, Pancreas
320	831094			755	928			HNFEO67	Colon, Breast/Ovarian

321	831099	fibronectin receptor beta subunit precursor (AA -20 to 778) [Homo sapiens] >pir|B27079|B27079 fibronectin receptor beta chain precursor - human >sp|P05556|ITB1_HUMAN FIBRONECTIN RECEPTOR BETA SUBUNIT PRECURSOR (INTEGRIN BETA-1) (CD29) (INTEGRIN VLA-4 BETA	gi|31442	3	1697	99	100	HA5AB03	Lung, Pancreas, Colon, Breast/Ovarian
322	831113	4E-binding protein 1 [Homo sapiens] >pir|S50866|S50866 4E-BP1 protein - human >pir|JC5899|JC5899 initiation factor 4E-binding protein 1 - human >sp|Q13541|Q13541 4E-BINDING PROTEIN 1. Length = 118	gi|561630	1	414	100	100	HMWHP74	Lung, Pancreas, Colon, Breast/Ovarian
323	831120			1	1221			HWLHY12	Pancreas, Colon
324	831172	Similarity to Human hnRNP F protein (PIR Acc. No. S43484);	gnl|PID|e1349655	2	721	52	66	HLWBE22	Pancreas, Breast/Ovarian
325	831178	(AF042501) cytochrome b [Homo sapiens] >sp|O78829|O78829 CYTOCHROME B (FRAGMENT). Length = 380	gi|3372365	512	829	69	70	HDLAG61	Lung, Colon
326	831184			770	1399			HWLGP91	Lung, Pancreas, Colon
327	831203			3	545			HMICQ42	Pancreas, Colon, Breast/Ovarian
328	831210	TGF-beta masking protein large subunit [Rattus norvegicus] >pir|A38261|A38261 masking protein precursor - rat Length = 1712	gi|207286	1	498	86	91	HMEIJ62	Pancreas, Colon
329	831228			104	214			HMEAM30	Lung, Pancreas, Breast/Ovarian

330	831256	MLN 64 [Homo sapiens] >dbj|D38255_1 CAB1 [Homo sapiens] >pir|I38027|I38027 MLN 64 protein - human >sp|Q14849|Q14849 MLN64 MRNA. Length = 445	gi|951279	658	1164	94	94	HMTBL29	Lung. Pancreas
331	831257	MLN 64 [Homo sapiens] >dbj|D38255_1 CAB1 [Homo sapiens] >pir|I38027|I38027 MLN 64 protein - human >sp|Q14849|Q14849 MLN64 MRNA. Length = 445	gi|951279	323	862	91	91	HLWDQ05	Pancreas, Colon
332	831277			3	1310			HUTHD56	Lung, Pancreas. Colon
333	831317	inter-alpha-trypsin inhibitor light chain [Homo sapiens] >gi|32047 HC polypeptide [Homo sapiens] >gi|24479 precursor polypeptide [Homo sapiens] >gi|825614 alpha1-microglobulin [Homo sapiens] >pir|S13433|HCHU alpha-1-microglobulin/inter-alpha-trypsin inhib	gi|186600	193	1290	100	100	HLQAC21	Pancreas. Breast/Ovarian
334	831339	(AB012276) ATFx [Mus musculus] >sp|O70191|O70191 ATFX (FRAGMENT). >sp|G246896|G246896 ATFX=ATF4 RELATED PROTEIN. {SUB 1-37} >sp|G246899|G246899 ATFX=ATF-4-RELATED PROTEIN. {SUB 38-76} Length = 84	gnl|PID|d1026241	631	1029	90	93	HLICC93	Lung, Colon, Breast/Ovarian
335	831363	acyl coenzyme A:cholesterol acyltransferase, carboxylesterase, ACAT {EC 2.3.1.26} {human, liver, Peptide, 568 aa] [Homo sapiens] >sp|G415564|G415564 CARBOXYLESTERASE {EC 3.1.1.1}. {SUB 20-568} >gi|179930 carboxylesterase [Homo sapiens] {SUB 62-568} Length	bbs|156481	123	1871	98	98	HLDNR55	Lung, Colon

336	831367	D-dopachrome tautomerase [Homo sapiens] >gi|1864028 D-dopachrome tautomerase [Homo sapiens] >gi|3047378 (AF058293) D-dopachrome tautomerase [Homo sapiens] >gnl|PID|e311354 phenylpyruvate tautomerase II |Homo sapiens| >gi|2352915 (AF012434) D-dopachrome ta	gi|1805303	325	618	100	100	HLDDR74	Lung, Colon
337	831379	cDNA from hypercalcemic tumour [Rattus norvegicus] >pir|S28223|S28223 parathyroid hormone-like protein - rat >sp|Q05310|L10K_RAT LEYDIG CELL TUMOR 10 KD PROTEIN. Length = 93	gi|57064	3	383	90	95	HKQAC03	Lung, Pancreas, Colon, Breast/Ovarian
338	831385			96	377			HKIMC75	Lung, Pancreas, Colon, Breast/Ovarian
339	831390	aldehyde reductase (EC 1.1.1.2) [Homo sapiens] >gi|2707824 (AF036683) aldehyde reductase [Homo sapiens] >pir|A33851|A33851 alcohol dehydrogenase (NADP+) (EC 1.1.1.2) - human >sp|G2707824|G2707824 ALDEHYDE REDUCTASE. >sp|P14550|ALDX_HUMAN ALCOHOL DEHYDROGE	gi|178481	254	1312	94	94	HKGDF04	Lung, Pancreas

340	831391	islet regenerating protein [Homo sapiens] >pir|A35197|RGHU1A regenerating islet lectin 1-alpha precursor - human >sp|P05451|LITA_HUMAN LITHOSTATHINE 1 ALPHA PRECURSOR (PANCREATIC STONE PROTEIN) (PSP) (PANCREATIC THREAD PROTEIN) (PTP) (ISLET OF LANGERHANS	gi|190979	71	592	100	100	HLDBE06	Pancreas. Colon
341	831405	factor H homologue [Homo sapiens] >pir|I56100|I56100 factor H homologue - human >sp|Q03591|CFH1_HUMAN COMPLEMENT FACTOR H-LIKE PROTEIN 1 PRECURSOR (H36). Length = 330	gi|183763	53	1078	94	94	HLDOB31	Lung. Pancreas. Colon. Breast/Ovarian
342	831442	PDGF associated protein [Homo sapiens] >sp|Q13442|HP28_HUMAN 28 KD HEAT- AND ACID-STABLE PHOSPHOPROTEIN (HASPP28) (PDGF ASSOCIATED PROTEIN). Length = 181	gi|1136584	2	595	60	60	HKAEB15	Lung. Pancreas. Colon. Breast/Ovarian
343	831476	dermatopontin [Homo sapiens] >pir|A47220|A47220 dermatopontin precursor - human >sp|Q07507|DERM_HUMAN DERMATOPONTIN PRECURSOR. >pir|S34838|S34838 tyrosine-rich acidic matrix protein - pig {SUB 101-144} Length = 201	gi|311614	1	630	91	91	HJMBK21	Lung. Pancreas. Colon
344	831488	similar to Saccharomyces cerevisiae Spt4; protein has potential N-terminal zinc-finger [Homo sapiens] >gi|1401053 SUPT4H [Homo sapiens] >gi|1401055 SUPT4H [Homo sapiens] >gi|1401066 Supt4h [Mus musculus] >gi|3779194 chromatin structural protein homolog [M	gi|1209779	158	580	100	100	HJBCG39	Colon. Breast/Ovarian

345	831518			240	467			HATCV09	Pancreas, Colon. Breast/Ovarian
346	831519	(AF062536) cullin 1 [Homo sapiens] >sp|O60719|O60719 CULLIN 1. >gi|4153866 (AC005229) cullin 1 [Homo sapiens] {SUB 1-263} Length = 776	gi|3139077	165	1712	100	100	HOECI49	Pancreas. Breast/Ovarian
347	831521			3	863			HIBCE91	Colon. Breast/Ovarian
348	831550	mel-13a protein - mouse Length = 132	pir|S65785|S65785	158	457	70	75	HCHNH46	Lung, Pancreas. Breast/Ovarian
349	831560			1474	1818			HCROA68	Pancreas. Breast/Ovarian
350	831562	fibromodulin [Homo sapiens] >sp|Q06828|FMOD_HUMAN FIBROMODULIN PRECURSOR (FM) (COLLAGEN-BINDING 59 KD PROTEIN). Length = 376	gi|297091	28	1272	90	91	HEGAD80	Pancreas. Breast/Ovarian
351	831570	(AF042822) epithin [Mus musculus] >sp|G4104970|G4104970 EPITHIN. Length = 902	gi|4104970	2	1861	77	85	HLWCC68	Lung. Pancreas. Colon
352	831593			726	878			HHBFW28	Lung, Pancreas
353	831596	32 kd accessory protein [Bos taurus] >gi|190376 proton ATPase accessory subunit [Homo sapiens] {SUB 264-351} Length = 351	gi|736727	2	808	100	100	HHEDJ61	Colon. Breast/Ovarian
354	831627			1	903			HBJHI46	Lung. Pancreas
355	831649			1	738			HFTDD09	Lung. Colon
356	831664	transformation upregulated nuclear protein - human Length = 464	pir|S43363|S43363	180	1574	94	94	HFPCU40	Lung. Colon

357	831674	complement protein C8 beta subunit precursor [Homo sapiens] >pir|A43071|C8HUB complement C8 beta chain precursor - human >sp|P07358|CO8B_HUMAN COMPLEMENT COMPONENT C8 BETA CHAIN PRECURSOR. Length = 591	gi|179720	1	1338	96	96	HLDOX36	Pancreas. Colon
358	831684	(AF053630) monocyte/neutrophil elastase inhibitor [Homo sapiens] >pir|S27383|S27383 elastase inhibitor - human >sp|P30740|ILEU_HUMAN LEUKOCYTE ELASTASE INHIBITOR (LEI) (MONOCYTE/NEUTROPHIL ELASTASE INHIBITOR) (EI). >sp|G2997692|G2997692 MONOCYTE/NEUTROPHI	gi|2997692	1	1311	96	96	HFOXE22	Pancreas. Colon
359	831687	Mpv17 [Mus musculus] >pir|S29031|S29031 mpv17 protein - mouse >sp|P19258|MPV1_MOUSE MPV17 PROTEIN. >gi|3252875 (AF038632) Mpv17 protein [Mus musculus] {SUB 155-176} Length = 176	gi|199790	60	305	89	93	HFKHD75	Pancreas. Colon
360	831726	rat ribosomal protein L36 [Rattus norvegicus] >pir|JN0483|JN0483 ribosomal protein L36 - rat Length = 105	gi|312345	77	454	98	98	HAGDQ96	Lung. Breast/Ovarian
361	831736			95	484			HLWEQ18	Colon. Breast/Ovarian
362	831762			37	720			HEQB179	Pancreas. Colon
363	831801	ear-2 gene product [Homo sapiens] >pir|S02709|S02709 ear-2 protein - human >sp|P10588|EAR2_HUMAN V-ERBA RELATED PROTEIN EAR-2. Length = 403	gi|31065	3	812	76	77	HKAHB85	Lung. Pancreas. Breast/Ovarian

364	831848			2018	2284			HE8AF82	Lung. Colon. Breast/Ovarian
365	831861	(AF076786) serum amyloid A-activating factor SAF-8 [Oryctolagus cuniculus] >sp|G3986442|G3986442 SERUM AMYLOID A-ACTIVATING FACTOR SAF-8 (FRAGMENT). Length = 214	gi|3986442	341	775	77	77	HJPCX51	Lung. Pancreas. Breast/Ovarian
366	831866	(AF054174) histone macroH2A1.2 [Homo sapiens] >sp|G3341992|G3341992 HISTONE MACROH2A1.2. Length = 371	gi|3341992	53	1186	100	100	HE6FG90	Lung. Colon
367	831878			2	661			HDTLN67	Colon. Breast/Ovarian
368	831899			1	693			HDTBQ51	Colon. Breast/Ovarian
369	831913	nuclear antigen H731 [Homo sapiens] >pir|JC5193|JC5193 nuclear protein H731 - human >sp|Q99834|Q99834 NUCLEAR ANTIGEN H731. Length = 458	gi|1825562	95	1132	96	97	HLYGA31	Lung. Colon
370	831972	p619 [Homo sapiens] >pir|S71752|S71752 giant protein p619 - human >sp|Q15751|Q15751 P619. Length = 4861	gi|1477565	331	855	33	58	HDPKK57	Lung. Pancreas. Breast/Ovarian
371	831985			425	805			HDPFP36	Lung. Pancreas. Colon. Breast/Ovarian
372	831986			30	467			HCHC1168	Pancreas. Colon. Breast/Ovarian
373	832010	(AL021918) b3418.1 (Kruppel related Zinc Finger protein 184) [Homo sapiens] >sp|O60792|O60792 B3418.1 (KRUPPEL RELATED ZINC FINGER PROTEIN 184). Length = 751	gnl|PID|e1293199	1	348	57	69	HDFUB44	Lung. Pancreas. Colon

374	832016	C protein (AA 1-159) [Homo sapiens] >pir|S01387|S01387 U1 snRNP protein C - human Length = 159	gi|37543	2	604	100	100	HTTDG34	Lung, Breast/Ovarian
375	832041	metalloelastase HME (EC 3.4.24.-) - human >sp|P39900|COGM_HUMAN MACROPHAGE METALLOELASTASE PRECURSOR (EC 3.4.24.65) (HME) (MATRIX METALLOPROTEINASE-12) (MMP-12). Length = 470	pir|A49499|A49499	54	1472	100	100	HDPGC33	Lung, Pancreas, Colon
376	832044	5-aminoimidazole-4-carboxamide-1-beta-D-ribonucl eotide transformylase/inosinicase [Homo sapiens] >gnl|PID|d1022617 5-aminoimidazole-4-carboxamide ribonucleotide transformylase [Homo sapiens] >pir|JC4642|JC4642 purH bifunctional enzyme - human >sp|Q13856|	gnl|PID|d1012226	1	1794	99	99	HGCOL40	Lung, Pancreas, Colon, Breast/Ovarian
377	832049	proteasome subunit HsC10-II [Homo sapiens] >pir|S55041|S55041 multicatalytic endopeptidase complex (EC 3.4.99.46) beta chain C10-II - human >sp|P49720|PRCT_HUMAN PROTEASOME THETA CHAIN (EC 3.4.99.46) (MACROPAIN THETA CHAIN) (MULTICATALYTIC ENDOPEPTIDASE C	gnl|PID|d1006190	84	710	99	100	HCFAU68	Lung, Pancreas, Breast/Ovarian
378	832122			427	846			HCUDT18	Lung, Pancreas, Colon, Breast/Ovarian
379	832148			246	380			HFTHN81	Colon, Breast/Ovarian
380	832197			433	642			HCQA1151	Pancreas, Breast/Ovarian
381	832237			290	553			HOCTE23	Lung, Colon
382	832246			66	959			HCMSD61	Lung, Pancreas

383	832256	ligand for eph-related receptor tyrosine kinases [Homo sapiens] >gi|1809292 putative EPH-related PTK receptor ligand LERK-8 [Homo sapiens] >sp|Q15768|EFB3_HUMAN EPHRIN-B3 PRECURSOR (EPH-RELATED RECEPTOR TYROSINE KINASE LIGAND 8) (LERK-8) (EPH-RELATED RECE	gi|1469782	1	81	100	100	HBXAC19	Pancreas, Colon, Breast/Ovarian
384	832280	(AF071747) topoisomerase II alpha [Homo sapiens] >sp|G3869316|G3869316 TOPOISOMERASE II ALPHA. Length = 1531	gi|3869316	2	1141	79	79	HNTSQ37	Lung, Colon, Breast/Ovarian
385	832285			1550	1783			HLTBQ50	Lung, Prostate
386	832294			1	666			HBMCR80	Lung, Colon
387	832326			472	1131			HJPAT43	Lung, Colon, Breast/Ovarian
388	832333	CENP-B protein [Ovis aries] >sp|P49451|CENB_SHEEP MAJOR CENTROMERE AUTOANTIGEN B (CENTROMERE PROTEIN B) (CENP-B) (FRAGMENT). Length = 239	gi|1016292	3	551	96	96	HCHMS55	Pancreas, Breast/Ovarian
389	832346			295	471			HBAGU45	Colon, Breast/Ovarian
390	832370	HER2 receptor [Homo sapiens] >gi|553282 c-erb-2 protein [Homo sapiens] {SUB 737-1031} >gi|553332 HER-2/neu [Homo sapiens] {SUB 1-191} >gi|183989 HER2 receptor (AA at 3) [Homo sapiens] {SUB 740-910} >gi|182169 c-erb B2/neu protein [Homo sapiens] {SUB 1081-	gi|306840	2	406	83	83	HFIEC83	Lung, Breast/Ovarian
391	832381			138	539			HATAA19	Pancreas, Breast/Ovarian

392	832394	platelet-endothelial tetraspan antigen 3 [Homo sapiens] >sp|P48509|C151_HUMAN PLATELET-ENDOTHELIAL TETRASPAN ANTIGEN 3 (PETA-3) (GP27) (MEMBRANE GLYCOPROTEIN SFA-1) (CD151 ANTIGEN). Length = 253	gi|541613	2	847	85	85	HFTTD21	Lung. Pancreas
393	832454	precursor polypeptide [Homo sapiens] >pir|A25971|C2HU complement C2 precursor - human >gi|187765 MHC complement component C2 [Homo sapiens] {SUB 21-46} Length = 752	gi|34628	160	357	100	100	HLQBT44	Prostate. Breast/Ovarian
394	832465			1	324			HAJBC51	Lung. Pancreas
395	832475	X box binding protein-1 [Homo sapiens] >pir|A36299|A36299 transcription factor hXBP-1 - human Length = 260	gi|306893	470	817	100	100	HTJMJ52	Pancreas. Breast/Ovarian
396	832495	EB1 [Homo sapiens] >pir|I52726|I52726 EB1 - human >sp|Q15691|Q15691 EB1. Length = 268	gi|998357	1	933	100	100	HADB85	Lung. Pancreas
397	832498	pyrroline-5-carboxylate synthase [Homo sapiens] >sp|G4097816|G4097816 PYRROLINE-5-CARBOXYLATE SYNTHASE. Length = 793	gi|4097816	2	1036	95	95	HLTGQ24	Lung. Pancreas
398	832501			736	996			HAGFI57	Lung. Pancreas. Colon
399	832505	protein synthesis factor [Homo sapiens] >sp|P47813|IF1A_HUMAN EUKARYOTIC TRANSLATION INITIATION FACTOR 1A (EIF-1A) (EIF-4C). {SUB 2-144} Length = 144	gi|306725	61	648	100	100	HRABV57	Lung. Pancreas. Prostate
400	832539	protein synthesis initiation factor 4A [Mus musculus] Length = 408	gi|673433	472	1125	93	93	HRABO69	Lung. Breast/Ovarian
401	832554	HsGCN1 [Homo sapiens] >sp|Q99736|Q99736 HSGCN1 (FRAGMENT). Length = 1928	gi|2282576	409	927	99	99	HCHOX71	Pancreas. Breast/Ovarian

402	832569			2	667			HFCAE43	Lung. Colon
403	832578	(AL023777) rna binding protein [Schizosaccharomyces pombe] >sp|O74978|O74978 RNA BINDING PROTEIN. Length = 276	gnl|PID|e1295805	123	956	40	64	HBBBD67	Pancreas. Colon. Breast/Ovarian
404	832615			630	992			H2CBK94	Lung. Colon
405	832620			190	297			H2CBG53	Colon. Breast/Ovarian
406	832632	(AC002388) 60S ribosomal protein L30 isolog [Arabidopsis thaliana] >sp|O22165|O22165 60S RIBOSOMAL PROTEIN L30 ISOLOG. Length = 159	gi|2344898	41	592	52	69	H2CBD94	Lung. Colon. Breast/Ovarian
407	832633	putative phospho-beta-glucosidase [Bacillus stearothermophilus] >pir|D49898|D49898 cellobiose phosphotransferase system celC - Bacillus stearothermophilus >sp|Q45401|Q45401 PUTATIVE PHOSPHO-BETA-GLUCOSIDASE. Length = 245	gi|466475	3	566	52	64	HWACF51	Pancreas. Breast/Ovarian
408	833483			2	604			HCFCK33	Lung. Breast/Ovarian
409	834574	similar to S. cerevisiae longevity-assurance protein 1 (SP:P38703) [Caenorhabditis elegans] >sp|Q17870|Q17870 SIMILAR TO S. CEREVISIAE LONGEVITY-ASSURANCE PROTEIN 1. Length = 362	gi|1123105	634	1431	44	59	HFIBE126	Lung. Pancreas. Colon. Breast/Ovarian
410	834859	acidic calponin [human, kidney, Peptide, 329 aa] [Homo sapiens] >pir|JC4501|JC4501 acidic calponin - human >sp|Q15417|Q15417 ACIDIC CALPONIN. Length = 329	bbs|174416	53	541	99	100	HSTAT70	Lung. Pancreas. Colon. Breast/Ovarian

411	834861	factor activating exoenzyme S [Bos taurus] >gi|189953 phospholipase A2 [Homo sapiens] >gi|899459 14-3-3 protein [Homo sapiens] >pir|A38246|PSHUAM 14-3-3 protein zeta - human >pir|A47389|A47389 14-3-3 protein zeta - bovine >sp|P29312|143Z_HUMAN 14-3-3 PROT	gi|163042	74	967	99	99	HBXFL41	Lung, Pancreas, Prostate, Breast/Ovarian
412	834890	TRANSCRIPTION FACTOR BTF3 (RNA POLYMERASE B TRANSCRIPTION FACTOR 3). Length = 204	sp|Q64152|BTF3_MOUSE	70	588	90	91	H2CBT12	Lung, Pancreas, Prostate, Breast/Ovarian
413	835079			151	348			HOELH62	Lung, Pancreas, Breast/Ovarian
414	835554	homologue to sec61 [Rattus rattus] Length = 476	gi|206886	121	1287	98	98	HOHBH04	Lung, Pancreas
415	835560			2	574			HE9NK60	Lung, Pancreas
416	835723	immunoglobulin M heavy chain [Homo sapiens] >gi|38408 immunoglobulin M heavy chain [Homo sapiens] >pir|S37768|S37768 Ig mu chain C region - human Length = 453	gi|38406	48	1421	100	100	HLYFY90	Lung, Pancreas, Prostate, Colon, Breast/Ovarian
417	835791	(AJ005890) JM1 [Homo sapiens] >sp|O60826|O60826 JM1 PROTEIN, COMPLETE CDS (CLONE LLNLC110M0111Q7 (RZPD BERLIN)AND LLNLC110K2140Q7 (RZPD BERLIN)). Length = 627	gnl|PID|e1289743	437	1177	87	87	HTXJH25	Pancreas, Breast/Ovarian
418	835817			1369	1554			HAJAZ17	Lung, Breast/Ovarian
419	835840			2	730			HHEOJ47	Lung, Pancreas
420	836048			2052	2276			HDQDV21	Lung, Prostate

421	836898	human P5 [Homo sapiens] >pir|JC4369|JC4369 P5 protein - human >sp|Q15084|ERP5_HUMAN PROBABLE PROTEIN DISULFIDE ISOMERASE P5 PRECURSOR (EC 5.3.4.1). Length = 440	gnl|PID|d1009061	3	1427	90	90	HW1PA75	Lung, Pancreas, Colon, Breast/Ovarian
422	836927	(AF027299) protein 4.1-G [Homo sapiens] >sp|O43491|O43491 PROTEIN 4.1-G. Length = 1005	gi|2739096	3	1196	84	84	HDTKY58	Lung, Pancreas
423	837344	S1R [Cowpox virus] >sp|O72763|O72763 S1R PROTEIN. Length = 210	gnl|PID|e1289272	38	658	48	58	HLDAG32	Lung, Prostate
424	837789	bikunin [Homo sapiens] >sp|O00271|O00271 BIKUNIN. Length = 252	gi|2065529	365	1231	91	91	HDABR73	Colon, Breast/Ovarian
425	838549	(AL023828) Y17G7B.14 [Caenorhabditis elegans] >sp|E1323274|E1323274 Y17G7B.14 PROTEIN. Length = 364	gnl|PID|e1323274	2	853	42	55	HDQDW56	Lung, Breast/Ovarian
426	838754			437	1198			HTEQK83	Lung, Pancreas, Breast/Ovarian
427	838768			570	770			HWBCW80	Lung, Pancreas, Breast/Ovarian
428	839486	fibronectin precursor [Homo sapiens] >gi|4096846 fibronectin [Homo sapiens] {SUB 76-454} >gi|4096848 fibronectin [Homo sapiens] {SUB 1892-2103} >gi|182706 fibronectin [Homo sapiens] {SUB 1921-2040} >gi|182684 fibronectin [Homo sapiens] {SUB 2233-2328} Len	gi|31397	2	493	98	98	HSLGC71	Lung, Breast/Ovarian
429	839561	p34 protein [Rattus sp.] >pir|S36779|S36779 ribosome-binding protein p34 - rat >sp|Q63742|Q63742 P34 PROTEIN. Length = 307	gnl|PID|d1003291	45	1133	86	88	HUVFB27	Lung, Pancreas, Prostate

430	839816	similar to plasmodium merozite surface antigen precursor (SP:P04933) [Caenorhabditis elegans] >sp|Q22585|Q22585 SIMILAR TO PLASMODIUM MEROZITE SURFACE ANTIGEN PRECURSOR. Length = 634	gi|1293808	1	432	46	61	HWADY11	Lung. Breast/Ovarian
431	840068	UMP-CMP kinase [Sus scrofa] >pir|JC4181|JC4181 cytidylate kinase (EC 2.7.4.14) - pig >sp|Q29561|KCY_PIG UMP-CMP KINASE (EC 2.7.4.14) (CYTIDYLATE KINASE) (DEOXYCYTIDYLATE KINASE). Length = 196	gnl|PID|d1006692	2	757	97	99	HE8EH64	Lung. Pancreas. Breast/Ovarian
432	840279	(AF062328) p120 catenin isoform 1AB [Homo sapiens] >sp|O60715|O60715 P120 CATENIN ISOFORMS 1AB, 2AB, 3AB AND 4AB. >gi|3152823 (AF062322) p120 catenin isoform 2AB [Homo sapiens] {SUB 55-962} >gi|3152855 (AF062338) p120 catenin isoform 3AB [Homo sapiens] {S	gi|3152835	219	1493	93	93	HSRBI81	Lung, Pancreas
433	840489	connective tissue growth factor [Homo sapiens] >gi|474934 connective tissue growth factor [Homo sapiens] >pir|A40551|A40551 connective tissue growth factor - human >sp|P29279|CTGF_HUMAN CONNECTIVE TISSUE GROWTH FACTOR PRECURSOR. >gi|984956 connective tiss	gi|180924	1038	1370	100	100	HOEMS29	Lung. Pancreas

434	840538	glycyl tRNA synthetase [Homo sapiens] >pir|A55314|A55314 glycine--tRNA ligase (EC 6.1.1.14) precursor - human >gi|600727 glycyl-tRNA synthetase [Homo sapiens] {SUB 55-739} >gi|3845409 (AC004976) glycyl tRNA synthetase [Homo sapiens] {SUB 348-739} Length =	gnl|PID|d1006904	1	2298	100	100	HYAAN81	Lung, Pancreas, Prostate, Breast/Ovarian
435	840545			145	1302			HMCFK75	Lung, Pancreas, Colon, Breast/Ovarian
436	840549			1	492			HWHGB33	Lung, Prostate
437	840551	IgG Fc binding protein [Homo sapiens] Length = 5405	gnl|PID|d1020288	3	1409	93	93	HWLKM77	Lung, Prostate, Colon
438	840557			346	1014			H6EDS19	Prostate, Colon
439	840561	putative [Mus musculus] >pir|S15785|S15785 heat-stable antigen-related hypothetical protein HSA-C - mouse >sp|Q61692|Q61692 HSA-C GENE CODING FOR HEAT STABLE ANTIGEN. Length = 141	gi|51442	385	495	48	72	HL1BZ07	Lung, Pancreas, Prostate, Colon, Breast/Ovarian
440	840562	(AB008549) type I procollagen C-proteinase enhancer protein [Homo sapiens] >gi|3135316 (AF053356) PCOLCE [Homo sapiens] >sp|O14550|O14550 TYPE I PROCOLLAGEN C-PROTEINASE ENHANCER PROTEIN. Length = 449	gi|2589011	103	1476	96	96	HSSDI65	Lung, Pancreas, Prostate, Colon
441	840564	PQ-rich protein [Homo sapiens] >pir|S58222|S58222 PQ-rich protein - human >sp|Q15184|Q15184 PQ-RICH PROTEIN. Length = 400	gi|929660	2	688	67	68	HPJDB01	Lung, Pancreas

442	840572	putative [Homo sapiens] >pir|I54339|I54339 prot-oncogene - human >sp|P35226|BMI1_HUMAN DNA-BINDING PROTEIN BMI-1. Length = 326	gi|291873	3	1172	95	95	HTGAZ34	Prostate, Colon
443	840600			3	119			HYABI30	Prostate, Breast/Ovarian
444	840604	Similarity to Mouse A-RAF proto-oncogene serine/threonine-protein kinase (SW:KRAA_MOUSE);	gnl|PID|e1344589	1	1359	82	87	HWLHN58	Lung, Pancreas, Prostate, Breast/Ovarian
445	840608	olfactomedin [Rana catesbeiana] >pir|A47442|A47442 olfactomedin precursor - bullfrog >sp|Q07081|OLFM_RANCA OLFACTOMEDIN PRECURSOR (OLFACTORY MUCUS PROTEIN). Length = 464	gi|294502	200	1549	55	75	HWLFY46	Pancreas, Colon
446	840620			776	1267			HTXGB37	Lung, Prostate
447	840625			138	257			HTXDT74	Lung, Prostate
448	840626	nicotinamide N-methyltransferase [Homo sapiens] >gi|1063610 nicotinamide N-methyltransferase [Homo sapiens] >pir|A54060|A54060 nicotinamide N-methyltransferase (EC 2.1.1.1) - human >sp|P40261|NNMT_HUMAN NICOTINAMIDE N-METHYLTRANSFERASE (EC 2.1.1.1). Lengt	gi|494989	485	1282	100	100	HULAS90	Lung, Pancreas, Prostate, Colon, Breast/Ovarian
449	840638			16	351			HTTDV02	Prostate, Breast/Ovarian
450	840649	BL34=B cell activation gene [human, Peptide, 196 aa] [Homo sapiens] >pir|I56165|I56165 B cell activation protein BL34 - human Length = 196	bbs|129951	1	651	100	100	HTWCY84	Lung, Prostate
451	840651			2	706			HTTAD76	Pancreas, Prostate

452	840666			2	826			HTOAF86	Lung, Prostate
453	840681			157	2187			HTAER63	Lung, Prostate
454	840682	siah binding protein 1 [Homo sapiens] >sp|Q99628|Q99628 SIAH BINDING PROTEIN 1 (FRAGMENT). Length = 541	gi|1809248	1	1734	99	99	HE9PW64	Lung, Breast/Ovarian
455	840684			3	539			HTGBT14	Pancreas, Prostate, Breast/Ovarian
456	840697			96	560			HTECA52	Lung, Prostate
457	840698	t-complex-type molecular chaperone TCP1 - human >gi|339211 t-complex 1 protein [Homo sapiens] {SUB 308-365} Length = 556	pir|S10486|S10486	507	1853	96	97	HDABW50	Pancreas, Prostate
458	840708			1200	1487			HTEAF73	Lung, Prostate
459	840714	(AF053304) mitotic checkpoint component Bub3 [Homo sapiens] >gi|2921873 (AF047472) spleen mitotic checkpoint BUB3 [Homo sapiens] >gi|3639060 (AF081496) kinetochore protein BUB3 [Homo sapiens] >sp|O43684|O43684 SPLEEN MITOTIC CHECKPOINT BUB3. Length = 328	gi|2981231	175	1170	100	100	HTEGU90	Lung, Pancreas, Prostate, Breast/Ovarian
460	840716	(AC005326) asparagine synthetase [Homo sapiens] >sp|G3341715|G3341715 ASPARAGINE SYNTHETASE. >gi|703119 asparagine synthetase [Homo sapiens] {SUB 1-83} Length = 561	gi|3341715	166	1860	94	94	HSYAJ64	Lung, Prostate, Colon, Breast/Ovarian
461	840721			2	1324			HSUSE92	Lung, Pancreas, Prostate, Colon

462	840735	(AC002425) Gene product with similarity to Rat P8 [Homo sapiens] >gi|3202004 (AF069073) P8 protein [Homo sapiens] >gi|3202006 (AF069074) P8 protein [Homo sapiens] >sp|O60356|O60356 GENE PRODUCT WITH SIMILARITY TO RAT P8. Length = 82	gi|2947054	111	392	64	64	HSRDN44	Lung, Pancreas, Prostate, Breast/Ovarian
463	840738			985	1230			HTOJK11	Prostate, Colon
464	840745	52-kD SS-A/Ro autoantigen [Homo sapiens] Length = 475	gi|338490	2	694	46	63	HSSGC06	Lung, Prostate, Colon
465	840747	(AC004522) Zn-alpha2-glycoprotein [Homo sapiens] >sp|O60386|O60386 ZN-ALPHA2-GLYCOPROTEIN. Length = 334	gi|3006228	368	877	95	95	HLDOL02	Lung, Pancreas, Breast/Ovarian
466	840756	(AB005624) rig-analog DNA-binding protein [Sus scrofa] >gi|306898 rig-analog protein (putative); putative [Homo sapiens] >gi|337416 human homologue of rat insulinoma gene (rig); putative [Homo sapiens] >gi|305361 Rig DNA-binding protein (putative); putati	gnl|PID|d1022359	148	480	97	97	HCHBQ33	Lung, Pancreas, Colon, Breast/Ovarian
467	840776	Notch3 [Homo sapiens] >sp|G2668592|G2668592 NOTCH3. Length = 2321	gi|2668592	2	364	82	82	HSKJZ22	Lung, Breast/Ovarian
468	840784	aldehyde dehydrogenase 6 [Homo sapiens] >pir|A55684|A55684 aldehyde dehydrogenase (NAD+) (EC 1.2.1.3) 6 precursor, salivary - human >sp|P47895|DHA6_HUMAN ALDEHYDE DEHYDROGENASE 6 (EC 1.2.1.5). Length = 512	gi|544482	1	618	94	95	HSKAC75	Lung, Prostate, Colon, Breast/Ovarian

469	840788	P1 gene for c subunit of human mitochondrial ATP synthase gene product [Homo sapiens] >gnl|PID|d1002920 ATP synthase subunit c precursor [Homo sapiens] >pir|S34066|S34066 H+-transporting ATP synthase (EC 3.6.1.34) lipid-binding protein P1 precursor, mitoc	gi|38430	59	484	85	85	HHFUM32	Lung, Prostate, Colon, Breast/Ovarian
470	840794			162	1646			HOHBT28	Lung, Pancreas, Prostate, Colon
471	840797	OSF-2p1 [Homo sapiens] >pir|S36111|S36111 osteoblast-specific factor 2 - human >sp|Q15064|Q15064 OSF-2P1. Length = 779	gnl|PID|d1003341	2	2371	93	93	HDTIM52	Pancreas, Breast/Ovarian
472	840799			292	510			HWBCI48	Lung, Pancreas, Colon, Breast/Ovarian
473	840818	translational initiation factor eIF-2, alpha subunit [Homo sapiens] >sp|P05198|IF2A_HUMAN EUKARYOTIC TRANSLATION INITIATION FACTOR 2 ALPHA SUBUNIT (EIF-2- ALPHA). {SUB 2-315} Length = 315	gi|181995	3	806	100	100	HHBHM68	Lung, Prostate
474	840822	fatty acid synthase [Homo sapiens] >pir|G01880|G01880 fatty-acid synthase (EC 2.3.1.85) - human >sp|Q16702|Q16702 FATTY ACID SYNTHASE (EC 2.3.1.85) (FATTY-ACID SYNTHASE). Length = 2509	gi|915392	1423	2367	93	93	HGBHX28	Lung, Prostate, Colon, Breast/Ovarian
475	840830	diubiquitin [Homo sapiens] >sp|O15205|O15205 DIUBIQUITIN. Length = 165	gnl|PID|e321293	1	573	99	99	HFXHP85	Pancreas, Prostate

476	840846	glutathione S-transferase Ha subunit 1 (EC 2.5.1.18) [Homo sapiens] >gi|306815 glutathione S-transferase (GST, EC 2.5.1.18) [Homo sapiens] >gi|306809 glutathione S-transferase [Homo sapiens] >bbs|76373 glutathione S-transferase Ha1 subunit (EC 2.5.1.18) [	gi|306810	144	833	95	95	HFVHP57	Prostate, Breast/Ovarian
477	840848	prohibitin [human, Peptide, 272 aa] [Homo sapiens] >pir|I52690|I52690 prohibitin - human >sp|P35232|PHB_HUMAN PROHIBITIN. Length = 272	bbs|85658	81	917	93	93	HHBHM75	Lung, Pancreas, Prostate, Breast/Ovarian
478	840860	NAP [Homo sapiens] >pir|S40510|S40510 nucleosome assembly protein 1-like 1 - human >sp|P55209|NPL1_HUMAN NUCLEOSOME ASSEMBLY PROTEIN 1-LIKE 1 (NAP-1 RELATED PROTEIN). Length = 391	gi|189067	92	1309	80	80	HDTLJ39	Lung, Pancreas, Colon, Breast/Ovarian
479	840861	(AL021546) Cytochrome C Oxidase Polypeptide VIa-liver precursor (EC 1.9.3.1) [Homo sapiens] >sp|O43714|O43714 CYTOCHROME C OXIDASE POLYPEPTIDE VIA-LIVER PRECURSOR (EC 1.9.3.1) (CYTOCHROME-C OXIDASE) (CYTOCHROME OXIDASE) (CYTOCHROME A(3)) (CYTOCHROME AA(3)	gnl|PID|e1248288	2	520	100	100	HFPBO29	Lung, Prostate, Breast/Ovarian
480	840871	DNA polymerase delta small subunit [Homo sapiens] >pir|I38950|I38950 DNA-directed DNA polymerase (EC 2.7.7.7) delta regulatory chain - human >sp|P49005|DPD2_HUMAN DNA POLYMERASE DELTA SMALL SUBUNIT (EC 2.7.7.7). Length = 469	gi|1008458	2	628	99	99	HSDJX61	Pancreas, Colon, Breast/Ovarian

481	840874	secreted cyclophilin-like protein [Homo sapiens] >gi|181335 cyclophilin B [Homo sapiens] {SUB 9-216} >gi|181250 cyclophilin [Homo sapiens] {SUB 10-216} Length = 216	gi|337999	1	873	94	94	HFTDK64	Lung. Prostate
482	840878	unknown [Homo sapiens] >sp|P41271|DAN_HUMAN ZINC FINGER PROTEIN DAN (N03). Length = 180	gnl|PID|d1006216	227	676	99	100	H2MBT19	Lung. Pancreas. Colon. Breast/Ovarian
483	840880			153	320			HFIXK16	Prostate. Colon. Breast/Ovarian
484	840884	mutY homolog [Homo sapiens] >sp|Q15830|Q15830 MUTY HOMOLOG. Length = 535	gi|1458228	108	1565	99	99	HIBCH18	Lung. Prostate
485	840907			103	366			HETAD58	Pancreas. Prostate
486	840926			76	1347			HEOMT66	Lung. Pancreas. Prostate
487	840932	ATP synthase beta subunit precursor [Homo sapiens] >pir|A33370|A33370 H+-transporting ATP synthase (EC 3.6.1.34) beta chain precursor. mitochondrial - human >sp|P06576|ATPB_HUMAN ATP SYNTHASE BETA CHAIN, MITOCHONDRIAL PRECURSOR (EC 3.6.1.34). >gi|28931 be	gi|179281	2	1675	93	93	HFIB389	Lung. Prostate
488	840940	carbonyl reductase [Sus scrofa] >pir|JN0703|JN0703 carbonyl reductase (NADPH) (EC 1.1.1.184) - pig >sp|Q29529|CBR2_PIG LUNG CARBONYL REDUCTASE [NADPH] (EC 1.1.1.184) (NADPH-DEPENDENT CARBONYL REDUCTASE) (LCR). Length = 244	gnl|PID|d1004479	277	678	61	76	HCHNJ32	Pancreas. Breast/Ovarian

489	840947			2	565			HEGAN45	Lung, Pancreas, Prostate, Breast/Ovarian
490	840959	signal peptidase complex 25 kDa subunit [Canis familiaris] >pir|A55012|A55012 signal peptidase 25k chain - dog Length = 226	gi|533111	2	712	99	99	HEDAD53	Lung, Pancreas, Prostate, Breast/Ovarian
491	840964			177	344			HE8UK92	Prostate, Colon
492	840979	transcription factor-like protein 4 - human Length = 298	pir|JC5333|JC5333	11	631	99	100	HE9HD45	Lung, Pancreas, Prostate, Colon
493	840984	p167 [Homo sapiens] >gnl|PID|d1010130 The KIAA0139 gene product is related to mouse centrosomin B. [Homo sapiens] >gi|2501783 translation initiation factor 3 large subunit [Homo sapiens] >sp|Q14152|Q14152 KIAA0139 PROTEIN. >gi|1399801 p167 [Homo sapiens]	gi|1808985	3	3017	91	91	HE8OC40	Lung, Pancreas, Prostate, Breast/Ovarian
494	840986			1	693			HE8TB60	Pancreas, Prostate, Colon
495	840988			1	465			HE8QQ04	Pancreas, Prostate, Breast/Ovarian
496	840990	(AB010415) dTDP-4-keto-L-rhamnose reductase [Actinobacillus actinomycetemcomitans] >sp|O66251|O66251 DTDP-4-KETO-L-RHAMNOSE REDUCTASE. Length = 294	gnl|PID|d1029073	157	1140	32	59	HE8AM92	Pancreas, Prostate
497	840992	nidogen gene product [Homo sapiens] Length = 1246	gnl|PID|e218221	3	194	96	98	HE8BX38	Lung, Prostate, Colon, Breast/Ovarian
498	841009	sin3 associated polypeptide p18 [Homo sapiens] >sp|O00422|O00422 SIN3 ASSOCIATED POLYPEPTIDE P18. Length = 153	gi|2108210	59	523	92	92	HDTGP88	Lung, Pancreas, Prostate, Colon, Breast/Ovarian

499	841012	ribosomal protein L39 [Homo sapiens] >gnl|PID|d1012131 ribosomal protein L39 [Homo sapiens] >gi|575382 ribosomal protein L39 [Rattus norvegicus] >pir|JC4229|R6RT39 ribosomal protein L39 - rat >pir|G02654|G02654 ribosomal protein L39 - human Length = 51	gi|1373419	2	217	100	100	HSKXP01	Lung, Pancreas, Breast/Ovarian	
500	841016	connexin 43 [Homo sapiens] >gi|29917 gap junction protein (AA 1-382) [Homo sapiens] >pir|A35853|A35853 gap junction protein Cx43, cardiac - human >sp|P17302|CXA1_HUMAN GAP JUNCTION ALPHA-1 PROTEIN (CONNEXIN 43) (CX43) (GAP JUNCTION 43 KD HEART PROTEIN). [	gi|181209	1	810	94	94	HDTDH13	Lung, Pancreas, Prostate, Colon	
501	841017			402	683			HE2AY01	Lung, Prostate	
502	841021			983	1357			HNAAE75	Lung, Pancreas, Colon, Breast/Ovarian	
503	841032	(AB000910) ribosomal protein [Sus scrofa] >gi|1684917 L44-like ribosomal protein [Homo sapiens] >gi|1666702 ribosomal protein [Mus musculus] >gi|206732 ribosomal protein L36a [Rattus norvegicus] >pir|A29820|R6RT36 ribosomal protein L36a - rat Length = 106	gnl|PID|d1019960	3	395	100	100	HDQAD36	Lung, Colon	
504	841051			656	880			HDPDC65	Lung, Pancreas	
505	841064	small subunit ribonucleotide reductase [Homo sapiens] >pir|S25854|S25854 ribonucleoside-diphosphate reductase (EC 1.17.4.1) small chain - human Length = 389	gi|36155	6	1244	96	96	HDPMF32	Prostate, Colon, Breast/Ovarian	

506	841069			81	809			HDPMJ48	Prostate, Breast/Ovarian
507	841072	regulatory protein [Mus musculus] >gi|452276 npdcf-1 [Mus musculus] >pir|I48691|I48691 regulatory protein - mouse >sp|Q64322|NPD1_MOUSE NPDC-1 PROTEIN PRECURSOR. Length = 332	gi|456107	162	1139	91	95	HDPGF81	Lung, Prostate, Colon, Breast/Ovarian
508	841078			521	706			HDPKD92	Pancreas, Prostate
509	841080	HCNGP gene product [Mus musculus] >pir|S26660|S26660 HCNGP protein - mouse >sp|Q02614|HCGP_MOUSE TRANSCRIPTIONAL REGULATOR PROTEIN HCNGP. Length = 308	gi|57912	1	936	88	88	HDPJR07	Prostate, Breast/Ovarian
510	841088	quinone oxidoreductase [Homo sapiens] >gi|516534 quinone oxidoreductase2 [Homo sapiens] >pir|A32667|A32667 NAD(P)H dehydrogenase (quinone) (EC 1.6.99.2) 2 - human Length = 231	gi|190818	320	1096	100	100	HDPFX64	Lung, Pancreas, Prostate, Breast/Ovarian
511	841092			1187	1402			HJMBH15	Lung, Colon
512	841095	L protein (AA 1-558) [Homo sapiens] >pir|A33616|A33616 heterogeneous ribonuclear particle protein L - human Length = 558	gi|32356	2	904	84	84	H2LAT51	Lung, Pancreas, Colon, Breast/Ovarian
513	841096	(AB013357) 49 kDa zinc finger protein [Mus musculus] Length = 460	gnl|PID|d1038083	510	1907	80	80	HCFLJ15	Lung, Pancreas, Breast/Ovarian
514	841102			2	256			HDLAV12	Lung, Pancreas, Prostate, Breast/Ovarian
515	841104	zinc finger protein [Homo sapiens] >pir|S35305|S35305 finger protein ZNF91 - human Length = 1191	gi|186774	712	2451	54	70	HDLAB16	Pancreas, Prostate, Breast/Ovarian
516	841108	factor XIII a subunit [Homo sapiens] Length = 732	gi|182309	3	1838	99	99	HDPFE82	Lung, Pancreas, Colon

517	841118			320	487			HDLAE34	Lung, Pancreas, Prostate
518	841119	C11 protein [Homo sapiens] >gi|1890300 eukaryotic release factor 1 [Homo sapiens] >gnl|PID|e118068 C11 protein [Mesocricetus auratus] >pir|S50853|S50853 translation releasing factor eRF-1 - human >sp|P46055|ERF1_HUMAN EUKARYOTIC PEPTIDE CHAIN RELEASE FACT	gnl|PID|e118910	123	1367	100	100	HDPAE95	Lung, Pancreas, Prostate
519	841124	similar to deoxyribose-phosphate aldolase [Caenorhabditis elegans] >sp|Q19264|DEOC_CAEEL PUTATIVE DEOXYRIBOSE-PHOSPHATE ALDOLASE (EC 4.1.2.4) (PHOSPHODEOXYRIBOALDOLASE) (DEOXYRIBOALDOLASE). Length = 303	gi|1019952	2	358	62	80	HDAAB17	Prostate, Colon
520	841137	(AF096285) serine-threonine kinase receptor-associated protein [Mus musculus] >sp|G4063383|G4063383 SERINE-THREONINE KINASE RECEPTOR-ASSOCIATED PROTEIN. Length = 351	gi|4063383	3	848	98	99	HDAAP84	Lung, Pancreas, Prostate, Breast/Ovarian
521	841143	fibrillarin [Homo sapiens] >pir|A38712|A38712 fibrillarin - human >gi|3399667 (AC005393) FBRL_HUMAN; 34 KD NUCLEOLAR SCLERODERMA ANTIGEN [Homo sapiens] {SUB 4-321} Length = 321	gi|31395	39	1040	100	100	HCRMJ87	Pancreas, Prostate, Breast/Ovarian
522	841148			2	1807			HCRNF38	Lung, Pancreas, Prostate, Colon, Breast/Ovarian
523	841149			324	797			HCRBS04	Prostate, Breast/Ovarian

524	841151	keratin [Carassius auratus] Length = 455	gi|212995	2	1399	45	64	HCRNY54	Lung, Pancreas, Prostate, Colon, Breast/Ovarian
525	841155			103	561			HCTIOF85	Prostate, Breast/Ovarian
526	841161	(AB014458) ubiquitin specific protease [Homo sapiens] >sp|D1035685|D1035685 UBIQUITIN SPECIFIC PROTEASE. Length = 785	gnl|PID|d1035685	3	1199	95	95	HCLCA56	Lung, Prostate
527	841162	set [Homo sapiens] >pir|A57984|A45018 template activating factor-I, splice form beta - human Length = 277	gi|338039	284	1063	99	100	HCWFR92	Prostate, Colon
528	841163	histone H2A [Mus musculus domesticus] >pir|S45110|S45110 histone H2A - mouse >sp|Q64426|Q64426 HISTONE H2A (FRAGMENT). Length = 137	gi|817939	201	665	100	100	HBMBF44	Pancreas, Breast/Ovarian
529	841169			21	440			HCFOF83	Lung, Prostate, Colon, Breast/Ovarian
530	841172	CLN3 protein [Homo sapiens] >gnl|PID|e283670 CLN3 protein [Homo sapiens] >gi|2947055 (AC002425) CLN3 [Homo sapiens] >gi|3337387 (AC002544) CLN [Homo sapiens] >gi|4102729 (AF015593) CLN3 protein [Homo sapiens] >pir|A57219|A57219 Batten disease-related prot	gi|1039423	291	740	100	100	HCHAG93	Prostate, Breast/Ovarian
531	841174	zinc finger protein 7 (ZFP7) [Homo sapiens] >pir|A34612|A34612 zinc finger protein ZNF7 - human Length = 686	gi|340446	3	386	98	98	HCHAW34	Prostate, Breast/Ovarian

532	841179	(AF069517) RNA binding protein DEF-3 [Homo sapiens] >sp|O75524|O75524 RNA BINDING PROTEIN DEF-3. Length = 1123	gi|3212101	549	1742	85	85	HCHBU86	Lung. Pancreas. Prostate
533	841183	keratin 18 [Homo sapiens] >gi|307081 keratin 18 precursor [Homo sapiens] >gi|34037 cytokeratin 18 [Homo sapiens] >pir|S05481|S05481 keratin 18, type I, cytoskeletal - human >sp|P05783|K1CR_HUMAN KERATIN, TYPE I CYTOSKELETAL 18 (CYTOKERATIN 18) (K18) (CK 1	gi|386844	1	501	80	92	HCHCE20	Lung. Pancreas. Prostate, Colon. Breast/Ovarian
534	841186	(AJ006215) CMP-N-acetylneuraminic acid synthetase [Mus musculus] >sp|O88719|O88719 CMP-N-ACETYLNEURAMINIC ACID SYNTHETASE (EC 2.7.7.43) (ACYLNEURAMINATE CYTIDYLYLTRANSFERASE) (CMP-SIALATE PYROPHOSPHORYLASE) (CMP-SIALATE SYNTHASE). Length = 432	gnl|PID|e1314953	78	1421	95	97	HCFCG26	Lung. Prostate
535	841204	similar to beta-mannosyltransferase [Caenorhabditis elegans] >sp|Q22797|Q22797 SIMILAR TO BETA-MANNOSYLTRANSFERASE. Length = 487	gi|470340	1	1407	51	72	HCEFZ02	Lung. Pancreas. Prostate. Colon
536	841206			251	1192			HCEEM52	Lung. Prostate
537	841207	(AF062484) SDP8 [Mus musculus] >sp|O70493|O70493 SDP8. Length = 165	gi|3126981	193	585	41	63	HMTAR23	Prostate. Colon
538	841211	(AC004908) zinc finger protein from gene of uncertain exon structure; similar to Q99676 (PID:g3025333) [Homo sapiens] Length = 430	gi|4159888	110	766	47	62	HCEDM42	Prostate. Breast/Ovarian

539	841225	membrane protein [Homo sapiens] >gi|1048989 CD9 antigen [Homo sapiens] >gi|34769 MRP-1 (motility related protein) [Homo sapiens] >bbs|131345 CD9 antigen [human, leukocytes, Peptide, 228 aa] [Homo sapiens] >pir|A46123|A40402 CD9 antigen - human >sp|P21926|	gi|508496	41	865	88	88	HCRBB01	Lung, Pancreas, Prostate, Colon
540	841229	P1cdc47 [Homo sapiens] >pir|S70583|S70583 CDC47 homolog - human >sp|P33993|MCM7_HUMAN DNA REPLICATION LICENSING FACTOR MCM7 (CDC47 HOMOLOG) (P1.1-MCM3). >gnl|PID|d1006386 hMCM2 [Homo sapiens] {SUB 177-719} Length = 719	gnl|PID|d1010177	1	2298	98	98	HCE1D58	Lung, Pancreas, Prostate, Breast/Ovarian
541	841237	NAD(P)H:menadione oxidoreductase [Homo sapiens] >gi|189292 NAD(P)H:quinone oxireductase [Homo sapiens] >pir|A41135|A30879 NAD(P)H dehydrogenase (quinone) (EC 1.6.99.2) 1 - human >sp|P15559|DHQU_HUMAN NAD(P)H DEHYDROGENASE (QUINONE) 1 (EC 1.6.99.2) (QUINON	gi|189246	141	1028	95	95	HBMTA19	Lung, Pancreas, Prostate, Colon, Breast/Ovarian
542	841241	Thy-1 [Homo sapiens] >pir|A02106|TDHU Thy-1 membrane glycoprotein precursor - human Length = 161	gi|339683	128	622	86	87	HBXFG67	Lung, Pancreas, Prostate, Breast/Ovarian
543	841259	(AD001528) spermidine aminopropyltransferase [Homo sapiens] >sp|O00544|O00544 SPERMIDINE AMINOPROPYLTRANSFERASE. Length = 366	gi|2198557	3	1199	93	93	HCEIC53	Lung, Pancreas, Prostate, Breast/Ovarian

544	841260	FKBP51 [Homo sapiens] >pir|JC5422|JC5422 FK506-binding protein, FKBP51 - human >sp|Q13451|FKB5_HUMAN 51 KD FK506-BINDING PROTEIN (FKBP51) (PEPTIDYL-PROLYL CIS-TRANS ISOMERASE) (EC 5.2.1.8) (PPIASE) (ROTAMASE) (54 KD PROGESTERONE RECEPTOR-ASSOCIATED IMMUNO	gi|1916641	3	863	88	91	HBODM14	Lung, Prostate
545	841264			1	618			HBJHU33	Lung, Pancreas, Prostate
546	841275	Lutheran blood group glycoprotein [Homo sapiens] >pir|I38000|I38000 Lutheran blood group glycoprotein precursor - human >sp|P50895|LU_HUMAN LUTHERAN BLOOD GROUP GLYCOPROTEIN PRECURSOR (B-CAM CELL SURFACE GLYCOPROTEIN) (AUBERGER B ANTIGEN) (F8/G253 ANTIGEN	gi|603560	2	1183	89	89	HBGMO35	Prostate, Breast/Ovarian
547	841311	(AF019661) zeta proteasome chain; PSMA5 [Mus musculus] >sp|G3805976|G3805976 ZETA PROTEASOME CHAIN. Length = 241	gi|3805976	45	836	100	100	HCFMY64	Lung, Pancreas, Prostate, Breast/Ovarian
548	841313	neuronal protein 15.6 [unidentified] >sp|O09111|O09111 NEURONAL PROTEIN 15.6. Length = 133	gnl|PID|e274746	11	544	75	82	HBGNM82	Lung, Prostate, Colon, Breast/Ovarian
549	841317			1155	1553			HAPSG63	Lung, Prostate
550	841322	unnamed protein product [unidentified] >gi|496609 basic transcripion factor 2, 44 kD subunit [Homo sapiens] >sp|Q13888|Q13888 BASIC TRANSCRIPION FACTOR 2, 44 KD SUBUNIT (BASIC TRANSCRIPTION FACTOR 2 P44) (FRAGMENT). >gi|1737212 basic transcription factor	gnl|PID|e306259	200	1402	95	95	HAMGE23	Pancreas, Prostate

551	841331			2	955			HHFJL19	Lung, Breast/Ovarian
552	841332	alpha-2-macroglobulin precursor [Homo sapiens] >pir|A94033|MAHU alpha-2-macroglobulin precursor - human >sp|P01023|A2MG_HUMAN ALPHA-2-MACROGLOBULIN PRECURSOR (ALPHA-2-M). >gi|825615 alpha2-macroglobulin [Homo sapiens] {SUB 672-746} Length = 1474	gi|177870	2	3856	98	98	HAPQO79	Lung, Prostate
553	841338			1139	1363			HAJBU58	Pancreas, Prostate
554	841345	yeast methionyl-tRNA synthetase homolog [Homo sapiens] >pir|JC5224|JC5224 methionine--tRNA ligase (EC 6.1.1.10) - human >gi|804996 mitoxantrone-resistance associated gene [Homo sapiens] {SUB 423-900} Length = 900	gnl|PID|e218477	2	2761	94	94	HAJAQ46	Lung, Pancreas, Prostate, Breast/Ovarian
555	841349			151	1578			HMWFM73	Lung, Pancreas, Prostate, Breast/Ovarian
556	841355	glucose regulated protein 94 (400 AA) [Mesocricetus auratus] >pir|A26258|A26258 endoplasmin - hamster (fragment) >sp|P08712|ENPL_MESAU ENDOPLASMIN (94 KD GLUCOSE-REGULATED PROTEIN) (GRP94) (FRAGMENT). Length = 400	gi|49628	2	562	96	99	HAJAA78	Prostate, Breast/Ovarian
557	841417	arginine-rich nuclear protein [Homo sapiens] >pir|A40988|A40988 54K arginine-rich nuclear protein - human >sp|Q05519|Q05519 ARGININE-RICH 54 KD NUCLEAR PROTEIN. Length = 484	gi|178997	708	1835	73	73	HNTCL10	Lung, Pancreas, Colon, Breast/Ovarian

558	841548			278	613			HBXDN79	Lung, Breast/Ovarian
559	841632	(AF073298) 4F5rel [Homo sapiens] >gi|3641536 (AF073297) 4F5rel [Mus musculus] >sp|O75918|O75918 4F5REL. >sp|O88891|O88891 4F5REL. Length = 59	gi|3641538	49	255	100	100	HTLGV25	Lung, Breast/Ovarian
560	841662	HYA22 protein - human Length = 338	pir|JC5707|JC5707	2	532	78	81	HLQCP61	Prostate, Colon
561	841771			901	1146			HSYDN46	Lung, Pancreas
562	841827	RTP [Homo sapiens] >gi|3046386 (AF004162) nickel-specific induction protein [Homo sapiens] >sp|Q92597|Q92597 RTP, COMPLETE CDS. Length = 394	gnl|PID|d1014198	358	1110	97	97	HHFDI26	Pancreas, Prostate
563	841835			1232	1612			HWLJT54	Lung, Pancreas, Prostate, Colon, Breast/Ovarian
564	842259			2	691			HHFGF52	Lung, Pancreas, Prostate, Colon
565	842463			600	836			HETJY08	Lung, Pancreas
566	842595	ERp28 [Homo sapiens] >sp|P30040|ER29_HUMAN ENDOPLASMIC RETICULUM PROTEIN ERP29 PRECURSOR (ERP31) (ERP28). >sp|E1314951|E1314951 ERP28 PRECURSOR. Length = 261	gnl|PID|e1314951	50	916	92	92	HUFAB73	Lung, Breast/Ovarian
567	842722			2	1465			HYABB24	Lung, Pancreas, Prostate, Breast/Ovarian
568	842815			780	971			HPMSG47	Pancreas, Colon
569	842818	(AF038954) vacuolar H(+)-ATPase subunit [Homo sapiens] >sp|O75348|O75348 VACUOLAR H(+)-ATPASE SUBUNIT. Length = 118	gi|3329378	91	477	79	79	HSKJF03	Lung, Pancreas, Prostate, Breast/Ovarian

570	843251	(AF057297) ornithine decarboxylase antizyme 2 [Homo sapiens] >gi|3766170 (AF057297) ornithine decarboxylase antizyme 2 [Homo sapiens] >sp|G3766170|G3766170 ORNITHINE DECARBOXYLASE ANTIZYME 2. >gnl|PID|d1020346 product is unknown; seizure-related gene [Mus	gi|3766170	215	745	92	92	HTLIF83	Lung. Breast/Ovarian
571	843422			563	898			HISCW60	Lung, Pancreas. Colon. Breast/Ovarian
572	843784			1307	1864			HCECS78	Lung. Pancreas
573	844017			243	566			HKABG31	Lung. Colon
574	844138	Epithelin 1 & 2 [Homo sapiens] >gi|3005730 (AF055008) epithelin 1 and 2 [Homo sapiens] >pir|JC1284|GYHU granulin precursor - human >sp|G3005730|G3005730 EPITHELIN 1 AND 2. Length = 593	gi|31193	104	1966	100	100	HDPWW59	Lung. Breast/Ovarian
575	844166	(AF039689) antigen NY-CO-7 [Homo sapiens] >sp|O60526|O60526 ANTIGEN NY-CO-7. Length = 303	gi|3170178	1	1020	94	94	HABAE22	Lung. Pancreas. Prostate. Breast/Ovarian
576	844194			3	707			HE8PB56	Lung. Pancreas. Prostate. Colon. Breast/Ovarian
577	844394			378	635			HHEUP26	Lung. Pancreas, Breast/Ovarian
578	844450	weak similarity to rat TEGT protein (GI:456207) [Caenorhabditis elegans] >sp|P91373|P91373 SIMILARITY TO RAT TEGT PROTEIN. Length = 342	gi|1825601	113	1165	61	78	HTXOX92	Lung. Pancreas
579	844534			2	244			HCE3I65	Lung. Pancreas. Breast/Ovarian

580	844535	isocitrate dehydrogenase (NADP+) [Homo sapiens] >pir|S57499|S57499 isocitrate dehydrogenase (NADP+) (EC 1.1.1.42) precursor, mitochondrial - human >sp|P48735|IDHP_HUMAN ISOCITRATE DEHYDROGENASE [NADP], MITOCHONDRIAL PRECURSOR (EC 1.1.1.42) (OXALOSUCCINATE	gi|872121	3	1454	96	96	HCWGE38	Lung, Breast/Ovarian
581	844644	(AJ002308) synaptogyrin 2 [Homo sapiens] >sp|O43760|O43760 SYNAPTOGYRIN 2. Length = 224	gnl|PID|e1254905	1	720	91	91	HDPBQ51	Lung, Breast/Ovarian
582	844653	immunoglobulin lambda light chain gene product [Homo sapiens] >pir|S25745|S25745 Ig lambda chain - human (fragment) Length = 226	gi|33718	1	732	89	91	HCRQC91	Lung, Pancreas, Colon
583	844659	cathepsin D [Homo sapiens] >gi|29678 precursor polypeptide (AA -20 to 392) [Homo sapiens] >gi|181180 preprocathepsin D [Homo sapiens] >pir|A25771|KTHUD cathepsin D (EC 3.4.23.5) precursor - human >sp|P07339|CATD_HUMAN CATHEPSIN D PRECURSOR (EC 3.4.23.5).	gi|179948	21	539	94	94	HLDDQ71	Lung, Breast/Ovarian
584	844796			2	1054			HE6BS09	Colon, Breast/Ovarian
585	844812	(AF040642) contains similarity to transacylases [Caenorhabditis elegans] >sp|O44793|O44793 C50D2.7 PROTEIN. Length = 895	gi|2746788	13	1542	33	59	HDPFV13	Lung, Pancreas
586	844894	E25B protein [Mus musculus] >sp|O89051|O89051 E25B PROTEIN. Length = 266	gi|3746127	66	1013	96	99	HCLBO47	Lung, Pancreas, Colon

587	845361	phosphoglycerate kinase (EC 2.7.2.3) [Homo sapiens] >gi|387021 phosphoglycerate kinase [Homo sapiens] >gi|35435 coding sequence [Homo sapiens] >pir|I59050|KIHUG phosphoglycerate kinase (EC 2.7.2.3) - human Length = 417	gi|387020	39	1232	100	100	HHEUJ91	Pancreas, Colon
588	845620			508	1254			HWHGQ46	Lung, Pancreas, Prostate, Breast/Ovarian
589	845639	leukocyte antigen F [Homo sapiens] >gi|3273731 (AF055066) MHC class I HLA-F [Homo sapiens] >pir|A60384|A60384 MHC class I histocompatibility antigen HLA-F alpha chain Dew3 precursor - human >sp|P30511|HLAF_HUMAN HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, F A	gi|312407	2	814	90	90	HCFNA68	Lung, Pancreas, Colon, Breast/Ovarian
590	845660	Cyr61 [Homo sapiens] >gnl|PID|e311857 Gig1 protein [Homo sapiens] >gi|2196782 (AF003594) growth-factor inducible immediate early gene product CYR61 [Homo sapiens] >gnl|PID|e1249319 hCYR61 protein [Homo sapiens] >sp|O00622|CYR6_HUMAN CYR61 PROTEIN PRECURSO	gi|2130527	1	1365	91	91	HKAJW79	Lung, Pancreas, Prostate, Breast/Ovarian
591	845720			1	261			HKDAF83	Lung, Breast/Ovarian
592	845785			180	509			HSODT09	Pancreas, Colon, Breast/Ovarian
593	845897			1369	1677			HADAB09	Pancreas, Breast/Ovarian

594	845922	beta actin [Ovis aries] >gi|2661136 (AF035774) beta actin [Equus caballus] >gi|3320892 (AF076190) beta-actin [Trichosurus vulpecula] >gi|177968 cytoplasmic beta actin [Homo sapiens] >gnl|PID|d1021082 (AB004047) beta-actin [Homo sapiens] >gi|28252 beta-act	gi|2182269	1	1239	100	100	HWLQQ65	Lung, Pancreas, Colon
595	846016	(AB005894) ecalectin [Homo sapiens] >sp|O75028|O75028 ECALECTIN. Length = 323	gnl|PID|d1032501	47	337	97	97	HDPIT90	Lung, Pancreas
596	846040	0-44 protein [Rattus sp.] >pir|I57612|I57612 Rat brain 0-44 mRNA, segment 2 - rat >sp|P38718|P044_RAT 0-44 PROTEIN. Length = 127	gi|203072	127	585	84	88	HLICQ57	Lung, Pancreas, Prostate, Colon, Breast/Ovarian
597	846073	protein p68 (AA 1-614) [Homo sapiens] >gi|35220 p68 protein (AA 1-614) [Homo sapiens] >gi|2599360 (AF015812) RNA helicase p68 [Homo sapiens] >pir|JC1087|JC1087 RNA helicase, ATP-dependent - human >sp|P17844|DDX5_HUMAN PROBABLE RNA-DEPENDENT HELICASE P68 (	gi|38318	23	1051	91	92	HCWDW01	Lung, Pancreas
598	846257			286	651			HPWDE09	Lung, Prostate
599	HTXPN06R			65	286			HTXPN06	Lung, Breast/Ovarian
600	H2LAQ12R			3	311	71	79	H2LAQ12	Pancreas, Colon
601	HWAFU16R	(AB000911) ribosomal protein [Sus scrofa] >gnl|PID|e1339008 (AL031228) dJ1033B10.4 (40S ribosomal protein S18 (RPS18, KE-3)) [Homo sapiens] >gi|198580 ribosomal protein [Mus musculus] >gi|433447 ribosomal protein S18 [Rattus rattus] >gi|3811382 (AF100956)	gnl|PID|d1019961	3	320	86	86	HWAFU16	Lung, Pancreas, Colon, Breast/Ovarian

602	HAEAM91R	(AB005218) L subunit of photosynthetic reaction center complex [Acidiphilium rubrum] >gnl|PID|d1026488 (AB005219) L subunit of photosynthetic reaction center complex [Acidiphilium angustum] >sp|O70105|O70105 L. SUBUNIT OF PHOTOSYNTHETIC REACTION CENTER COM	gnl|PID|d1026481	174	215	66	66	HAEAM91	Pancreas, Colon, Breast/Ovarian
603	HOEMT44R	(AB010959) natural killer cell enhancing factor [Cyprinus carpio] Length = 199	gnl|PID|d1033048	54	431	84	93	HOEMT44	Lung, Colon, Breast/Ovarian
604	HE2OW04R	(AF001631) glucose-regulated protein GRP94 [Oryctolagus cuniculus] >sp|O18750|ENPL_RABIT ENDOPLASMIN (94 KD GLUCOSE-REGULATED PROTEIN) (GRP94) (FRAGMENT). Length = 716	gi|2581793	7	297	87	89	HE2OW04	Lung, Colon
605	HFCFG25R	(AF012422) ribosomal protein 46 [Drosophila melanogaster] Length = 51	gi|2307014	3	143	65	87	HFCFG25	Lung, Colon, Breast/Ovarian
606	HAPQP94R	(AF018432) dUTPase [Homo sapiens] >gi|1144332 deoxyuridine nucleotidohydrolase [Homo sapiens] >gi|1421818 deoxyuridine triphosphatase [Homo sapiens] >pir|G02777|G02777 dUTP pyrophosphatase (EC 3.6.1.23) - human >gi|292877 dUTP nucleotidohydrolase [Homo sa	gi|2443581	3	320	97	97	HAPQP94	Lung, Pancreas, Colon
607	H2CBI37R	(AF042107) ribosomal protein S3a [Eimeria tenella] >gi|2792508 (AF042107) ribosomal protein S3a [Eimeria tenella] Length = 264	gi|2792508	3	182	64	64	H2CBI37	Colon, Breast/Ovarian
608	HEOPQ13R	(AF042505) cytochrome b [Homo sapiens] >sp|G3372377|G3372377 CYTOCHROME B (FRAGMENT). Length = 380	gi|3372377	82	216	80	82	HEOPQ13	Lung, Colon

609	HCRNC25R	(AF051894) 15 kDa selenoprotein [Homo sapiens] Length = 161	gi|3095111	61	162	100	100	HCRNC25	Lung, Pancreas, Colon
610	HFITF28R	(AF056218) superficial zone protein [Bos taurus] >sp|O77765|O77765 SUPERFICIAL ZONE PROTEIN (FRAGMENT). Length = 401	gi|3676501	3	185	73	80	HFITF28	Pancreas, Colon
611	H2LAY26R			24	155			H2LAY26	Pancreas, Colon
612	HAPQA06R	40-kDa keratin protein [Homo sapiens] >pir|A31370|KRHU9 keratin 19, type I, cytoskeletal - human Length = 400	gi|386803	2	355	62	62	HAPQA06	Lung, Pancreas, Colon, Breast/Ovarian
613	HAQBM72R	40-kDa keratin protein [Homo sapiens] >pir|A31370|KRHU9 keratin 19, type I, cytoskeletal - human Length = 400	gi|386803	2	145	81	81	HAQBM72	Pancreas, Colon
614	HBGOK18R	40-kDa keratin protein [Homo sapiens] >pir|A31370|KRHU9 keratin 19, type I, cytoskeletal - human Length = 400	gi|386803	1	429	91	92	HBGOK18	Lung, Pancreas, Colon, Breast/Ovarian
615	H2MAC07R	acidic ribosomal phosphoprotein (P1) [Homo sapiens] >pir|B27125|R6HUP1 acidic ribosomal protein P1 - human Length = 114	gi|190234	111	458	100	100	H2MAC07	Lung, Colon, Breast/Ovarian
616	HTWKF26R	acidic ribosomal phosphoprotein (P2) [Homo sapiens] >pir|C27125|R6HUP2 acidic ribosomal protein P2 - human Length = 115	gi|190236	1	345	95	96	HTWKF26	Lung, Pancreas, Breast/Ovarian
617	HTAHR89R	ADP,ATP carrier protein T2 - human >sp|P12236|ADT3_HUMAN ADP,ATP CARRIER PROTEIN, LIVER ISOFORM T2 (ADP/ATP TRANSLOCASE 3) (ADENINE NUCLEOTIDE TRANSLOCATOR 3) (ANT 3). Length = 298	pir|S03894|S03894	13	408	96	96	HTAHR89	Lung, Pancreas

618	HOACE24R	alcohol dehydrogenase [Homo sapiens] >pir|A33371|DEHUE1 aldehyde dehydrogenase (NAD+) (EC 1.2.1.3) 1, cytosolic - human >sp|P00352|DHAC_HUMAN ALDEHYDE DEHYDROGENASE, CYTOSOLIC (EC 1.2.1.3) (CLASS 1) (ALHDII) (ALDH-E1). {SUB 2-501} Length = 501	gi|178372	3	374	91	92	HOACE24	Pancreas, Colon
619	HOELC27R	aldolase A (EC 4.1.3.13) [Homo sapiens] >gi|28597 aldolase A (AA 1-364) [Homo sapiens] >pir|S14084|ADHUA fructose-bisphosphate aldolase (EC 4.1.2.13) A - human >sp|P04075|ALFA_HUMAN FRUCTOSE-BISPHOSPHATE ALDOLASE A (EC 4.1.2.13) (MUSCLE-TYPE ALDOLASE). {S	gi|178351	68	604	100	100	HOELC27	Lung, Pancreas, Breast/Ovarian
620	HWLBS25R	aldolase A [Gallus gallus] >gi|409193 aldolase A [Gallus gallus] >bbs|167536 aldolase C=fructose-1,6-biphosphate aldolase {EC 4.1.2.13} [chickens, brain, Peptide Partial, 42 aa] [Gallus gallus] >pir|I51291|I51291 aldolase C - chicken (fragment) Length = 4	gi|409191	3	95	90	93	HWLBS25	Lung, Pancreas, Colon, Breast/Ovarian
621	HWLVW62R	alpha-1 type III collagen [Homo sapiens] Length = 345	gi|180414	1	213	97	97	HWLVW62	Lung, Colon, Breast/Ovarian
622	HALSE08R	ALPHA-1-ANTICHYMOTRYPSIN PRECURSOR (ACT). >gi|4165890 (AF089747) alpha-1-antichymotrypsin precursor [Homo sapiens] {SUB 17-423} >gi|177933 alpha-1-antichymotrypsin precursor [Homo sapiens] {SUB 22-423} >gi|28332 alpha 1 antichymotrypsin [Homo sapiens] {SU	sp|P01011|AACT_HUMAN	3	233	95	97	HALSE08	Lung, Pancreas

623	HFKHD94R	alpha-2 chain precursor (AA -25 to 1018) (3416 is 2nd base in codon) [Homo sapiens] Length = 1043	gi|30076	2	316	97	97	HFKHD94	Pancreas, Breast/Ovarian
624	HCE2M86R	alpha-adaptin (A) (AA 1-977) [Mus musculus] >pir|A30111|A30111 alpha-adaptin A - mouse >sp|P17426|ADAA_MOUSE ALPHA-ADAPTIN A (CLATHRIN ASSEMBLY PROTEIN COMPLEX 2 ALPHA-A LARGE CHAIN) (100 KD COATED VESICLE PROTEIN A) (PLASMA MEMBRANE ADAPTOR HA2/AP2 ADAPT	gi|49878	58	165	75	80	HCE2M86	Lung, Colon, Breast/Ovarian
625	HOFOA89R	annexin IV (placental anticoagulant protein II) [Homo sapiens] >gnl|PID|d1011889 annexin IV (carbohydrtate-binding protein p33/41) [Homo sapiens] >pir|A42077|A42077 annexin IV - human >sp|P09525|ANX4_HUMAN ANNEXIN IV (LIPOCORTIN IV) (ENDONEXIN I) (CHROMOB	gi|178699	154	399	94	94	HOFOA89	Pancreas, Colon, Breast/Ovarian
626	HBWCN69R	beta-1,2-N-acetylglucosaminyltransferase II [Homo sapiens] >pir|S66256|S66256 alpha-1,6-mannosyl-glycoprotein beta-1, 2-N-acetylglucosaminyltransferase (EC 2.4.1.143) - human >sp|Q10469|GNT2_HUMAN ALPHA-1,6-MANNOSYL-GLYCOPROTEIN BETA-1,2-N-ACETYLGLUCOSAM	gi|902745	60	308	88	90	HBWCN69	Pancreas, Colon
627	HLQGB43R	beta-2-microglobulin [Homo sapiens] Length = 119	gi|179318	1	78	100	100	HLQGB43	Lung, Pancreas, Colon
628	HCROL58R			3	506			HCROL58	Pancreas, Colon
629	HS2IF12R			83	475			HS2IF12	Pancreas, Colon
630	HWLWA01R			2	538			HWLWA01	Pancreas, Colon

631	HCHMV24R							HCHMV24	Pancreas, Colon, Breast/Ovarian
632	HCHPT49R							HCHPT49	Colon, Breast/Ovarian
633	HCRMG12R							HCRMG12	Pancreas, Colon
634	HWLWE68R							HWLWE68	Pancreas, Colon
635	HCHPF59R							HCHPF59	Pancreas, Breast/Ovarian
636	HS2IA81R							HS2IA81	Pancreas, Colon
637	HCRNC17R							HCRNC17	Pancreas, Colon
638	HISDJ39R							HISDJ39	Pancreas, Colon
639	HWLEL43R							HWLEL43	Pancreas, Colon
640	HASCG71R							HASCG71	Lung, Colon, Breast/Ovarian
641	HOEMO43R							HOEMO43	Lung, Pancreas, Colon, Breast/Ovarian
642	HRDFT95R	c-erb-B-2 precursor [Homo sapiens] >pir|A24571|A24571 protein-tyrosine kinase (EC 2.7.1.112) erbB2 precursor - human >sp|P04626|ERB2_HUMAN ERBB-2 RECEPTOR PROTEIN-TYROSINE KINASE PRECURSOR (EC 2.7.1.112) (P185ERBB2) (NEU PROTO-ONCOGENE) (C-ERBB-2). Length	gi|31198	151	231	76	82	HRDFT95	Pancreas, Colon
643	HAGEP27R	C10 protein [Bos taurus] >pir|A38464|A38464 33K laminin receptor homolog - bovine Length = 295	gi|163303	3	137	86	86	HAGEP27	Lung, Pancreas, Colon, Breast/Ovarian

644	HSYDG18R	calmodulin [Homo sapiens] >sp|Q13942|Q13942 CALMODULIN. >pir|A56785|A56785 calmodulin - pig (fragment) {SUB 80-130} >gi|3243222 (AF069912) calmodulin [Xiphias gladius] {SUB 80-114} >pir|E44101|E44101 calmodulin, vasoactive intestinal peptide-binding prote	gi|825635	3	422	100	100	HSYDG18	Lung. Pancreas. Colon
645	HLJDZ15R	cathepsin C [Homo sapiens] >gi|1947071 prepro dipeptidyl peptidase I [Homo sapiens] >pir|S66504|S66504 dipeptidyl-peptidase I (EC 3.4.14.1) precursor - human >sp|P53634|CATC_HUMAN DIPEPTIDYL-PEPTIDASE I PRECURSOR (EC 3.4.14.1) (DPP-I) (CATHEPSIN C) (CATHE	gi|1006657	3	110	71	77	HLJDZ15	Lung. Colon
646	HAHDQ54R	cathepsin D [Homo sapiens] >gi|29678 precursor polypeptide (AA -20 to 392) [Homo sapiens] >gi|181180 preprocathepsin D [Homo sapiens] >pir|A25771|KHHUD cathepsin D (EC 3.4.23.5) precursor - human >sp|P07339|CATD_HUMAN CATHEPSIN D PRECURSOR (EC 3.4.23.5).	gi|179948	2	103	100	100	HAHDQ54	Lung. Pancreas
647	HTLHI18R	collagen alpha 2(VI) chain precursor, long splice form - human >gi|179711 alpha-2 collagen type VI-a' [Homo sapiens] {SUB 590-1018} >gi|291918 alpha-2 type VI collagen [Homo sapiens] {SUB 315-358} Length = 1018	pir|S05378|CGHU2A	2	481	89	89	HTLHI18	Lung, Pancreas

648	HACAC47R	complement component C3 [Homo sapiens] >pir|A94065|C3HU complement C3 precursor - human >sp|P01024|CO3_HUMAN COMPLEMENT C3 PRECURSOR [CONTAINS: C3A ANAPHYLATOXIN]. >gi|181130 complement component C3 [Homo sapiens] {SUB 1-24} Length = 1663	gi|179665	1	315	79	80	HACAC47	Lung, Pancreas, Breast/Ovarian
649	HLQFY41R	complement component C3 [Homo sapiens] >pir|A94065|C3HU complement C3 precursor - human >sp|P01024|CO3_HUMAN COMPLEMENT C3 PRECURSOR [CONTAINS: C3A ANAPHYLATOXIN]. >gi|181130 complement component C3 [Homo sapiens] {SUB 1-24} Length = 1663	gi|179665	3	377	96	98	HLQFY41	Lung, Pancreas, Colon, Breast/Ovarian
650	HOFMO83R	cyclin G [Homo sapiens] >gi|1236233 cyclin G1 [Homo sapiens] >gi|1236913 cyclin G1 [Homo sapiens] >pir|G02401|G02401 cyclin G1 - human >sp|P51959|CG2G_HUMAN G2/MITOTIC-SPECIFIC CYCLIN G1. >gnl|PID|d1013694 cyclin G [Homo sapiens] {SUB 1-279} >gi|1486361 c	gnl|PID|d1012016	2	205	87	93	HOFMO83	Pancreas, Breast/Ovarian
651	HFTDR22R	cytochrome b5, hepatic - brown howler monkey (fragment) Length = 87	pir|S07959|S07959	136	357	100	100	HFTDR22	Pancreas, Colon, Breast/Ovarian
652	HPJCZ01R	cytochrome c oxidase II [Macaca fascicularis] >pir|A27420|A27420 cytochrome-c oxidase (EC 1.9.3.1) chain II - crab-eating macaque mitochondrion (SGC1) >sp|P11948|COX2_MACFA CYTOCHROME C OXIDASE POLYPEPTIDE II (EC 1.9.3.1). Length = 227	gi|342255	2	163	44	50	HPJCZ01	Lung, Pancreas, Colon

653	HOEKC39R	cytochrome oxidase I [Homo sapiens] >gi|506829 cytochrome oxidase subunit I [Homo sapiens] >pir|A00463|ODHU1 cytochrome-c oxidase (EC 1.9.3.1) chain I - human mitochondrion (SGC1) >sp|P00395|COX1_HUMAN CYTOCHROME C OXIDASE POLYPEPTIDE I (EC 1.9.3.1). Leng	gi|13006	54	167	91	95	HOEKC39	Lung, Pancreas, Colon
654	HOELI24R	cytochrome oxidase subunit 3 [Homo sapiens] Length = 260	gi|2052365	29	166	97	97	HOELI24	Lung, Pancreas, Colon
655	HODE118R	cytochrome oxidase subunit II [Homo sapiens] >gi|530071 cytochrome oxidase subunit II [Homo sapiens] >gi|530073 cytochrome oxidase subunit II [Homo sapiens] >gi|530077 cytochrome oxidase subunit II [Homo sapiens] >gi|337187 cytochrome oxidase subunit II [	gi|530069	1	180	69	72	HODE118	Lung, Pancreas, Colon
656	HOSNR06R	cytochrome oxidase subunit II [Homo sapiens] >gi|530071 cytochrome oxidase subunit II [Homo sapiens] >gi|530073 cytochrome oxidase subunit II [Homo sapiens] >gi|530077 cytochrome oxidase subunit II [Homo sapiens] >gi|337187 cytochrome oxidase subunit II [	gi|530069	269	403	93	95	HOSNR06	Lung, Pancreas
657	HCQDL20R	cytochrome P450 PCN3 [Homo sapiens] >pir|A34101|A34101 cytochrome P450 3A5 - human >sp|P20815|CP35_HUMAN CYTOCHROME P450 3A5 (EC 1.14.14.1) (CYPIIIA5) (P450-PCN3). >gi|950342 cytochrome P450 [Homo sapiens] {SUB 1-24} Length = 502	gi|181346	39	245	98	98	HCQDL20	Pancreas, Colon

658	HTOHI64R	cytokeratin 15 (AA 1 - 456) [Homo sapiens] >pir|S01069|KRHU5 keratin 15, type I, cytoskeletal - human >sp|P19012|K1CO_HUMAN KERATIN, TYPE I CYTOSKELETAL 15 (CYTOKERATIN 15) (K15) (CK 15). Length = 456	gi|34071	149	253	89	89	HTOHI64	Prostate, Breast/Ovarian
659	HCHBR11R	cytokeratin 8 [Homo sapiens] Length = 483	gi|181400	3	380	55	57	HCHBR11	Lung, Pancreas, Colon, Breast/Ovarian
660	HADBE77R	cytoplasmic chaperonin hTRiC5 [Homo sapiens] Length = 201	gi|609308	43	294	80	84	HADBE77	Lung, Pancreas, Colon, Breast/Ovarian
661	HFKHD49R	D-beta-hydroxybutyrate dehydogenase [Rattus norvegicus] Length = 93	gi|930260	1	210	100	100	HFKHD49	Lung, Colon, Breast/Ovarian
662	HOEMJ59R	decorin [Homo sapiens] >gi|609452 decorin [Homo sapiens] {SUB 1-70} Length = 347	gi|181519	3	128	72	75	HOEMJ59	Lung, Colon
663	HTYNC43R	elongation factor 1-alpha 1 [Homo sapiens] >gi|927067 longation factor 1-alpha 1 [Homo sapiens] >pir|I59399|I59399 oncogene PTI-1 - human >sp|Q16577|Q16577 ONCOGENE. Length = 398	gi|927065	2	217	92	94	HTYNC43	Lung, Pancreas, Colon
664	H6EAQ15R	elongation factor 2 [Homo sapiens] >gi|31108 human elongation factor 2 [Homo sapiens] >pir|S18294|EFHU2 translation elongation factor eEF-2 - human >sp|P13639|EF2_HUMAN ELONGATION FACTOR 2 (EF-2). >gi|181969 elongation factor 2 [Homo sapiens] {SUB 501-858	gi|31106	2	70	100	100	H6EAQ15	Lung, Pancreas, Breast/Ovarian

665	HCFLM34R	elongation factor Tu [Mus musculus] >sp|Q61511|Q61511 EUKARYOTIC TRANSLATION ELONGATION FACTOR 1 ALPHA 1 (EEF-TU GENE ENCODING ELONGATION FACTOR TU, 5' END) (FRAGMENT). Length = 108	gi|553907	48	308	94	95	HCFLM34	Lung, Breast/Ovarian
666	HTTID16R	ENA-78 prepeptide [Homo sapiens] >gi|607031 neutrophil-activating peptide 78 [Homo sapiens] >gi|471243 ENA-78 gene product [Homo sapiens] >pir|JC2433|A55010 neutrophil-activating peptide ENA-78 - human >sp|P42830|EN78_HUMAN NEUTROPHIL ACTIVATING PROTEIN E	gi|684922	2	331	85	85	HTTID16	Pancreas, Colon
667	HDPAI45R	endoglin [Homo sapiens] >pir|S37628|S37628 endoglin - human Length = 625	gi|402207	2	181	65	65	HDPAI45	Pancreas, Colon
668	HKIXL19R	epoxide hydrolase [Homo sapiens] >gi|340390 epoxide hydrolase [Homo sapiens] >gi|34543 epoxide hydrolase (AA 1-455) [Homo sapiens] >gi|458701 epoxide hydrolase [Homo sapiens] >pir|A29939|A29939 epoxide hydrolase (EC 3.3.2.3) 1, microsomal - human >sp|P070	gi|450271	1	348	100	100	HKIXL19	Lung, Pancreas, Colon
669	H2LAY52R	EWS gene product [Mus musculus] >pir|A55726|A55726 RNA-binding protein Ews - mouse >sp|Q61545|EWS_MOUSE RNA-BINDING PROTEIN EWS. Length = 655	gi|488513	27	494	100	100	H2LAY52	Lung, Pancreas, Colon, Breast/Ovarian
670	HAJRB09R	FAST kinase [Homo sapiens] >pir|I37386|I37386 FAST kinase - human >sp|Q14296|Q14296 FAST KINASE. Length = 549	gi|1006659	19	324	77	77	HAJRB09	Pancreas, Colon

671	HAPNI86R	G9a [Homo sapiens] >pir|S30385|S30385 G9a protein - human >sp|Q14349|Q14349 G9A PROTEIN CONTAINING ANKYRIN-LIKE REPEATS. Length = 1001	gi|287865	3	419	97	97	HAPNI86	Lung, Colon
672	HCEVB92R	glutamate dehydrogenase [Homo sapiens] >sp|Q14400|Q14400 GLUTAMATE DEHYDROGENASE (FRAGMENT). Length = 258	gi|183056	2	217	78	81	HCEVB92	Pancreas, Colon
673	HAPRJ22R	glutamate--ammonia ligase [Homo sapiens] >pir|S18455|AJHUQ glutamate--ammonia ligase (EC 6.3.1.2) - human Length = 373	gi|31831	168	431	100	100	HAPRJ22	Lung, Pancreas, Prostate, Colon, Breast/Ovarian
674	HCRMZ32R	glutamine:fructose-6-phosphate amidotransferase [Homo sapiens] >pir|A45055|A45055 glutamine--fructose-6-phosphate transaminase (isomerizing) (EC 2.6.1.16) - human >sp|Q06210|GFAT_HUMAN GLUCOSAMINE--FRUCTOSE-6-PHOSPHATE AMINOTRANSFERASE [ISOMERIZING] (EC 2	gi|183082	2	316	91	91	HCRMZ32	Pancreas, Colon, Breast/Ovarian
675	HBMVM42R	guanine nucleotide regulatory protein [Homo sapiens] >gi|3041860 (AC004534) guanine nucleotide regulatory protein [Homo sapiens] >pir|I38402|I38402 guanine nucleotide regulatory protein - human >sp|Q12774|Q12774 GUANINE NUCLEOTIDE REGULATORY PROTEIN. Leng	gi|484102	1	363	84	87	HBMVM42	Colon, Breast/Ovarian

676	HADGE45R	guanine nucleotide-binding protein G-s-alpha-4 [Homo sapiens] >gi|31913 alpha-S1 (AA 1-380) [Homo sapiens] >pir|C31927|RGHUA1 GTP-binding regulatory protein Gs alpha chain (adenylate cyclase-stimulating), splice form 1 - human Length = 380	gi|386746	2	439	96	96	HADGE45	Lung, Pancreas, Colon
677	HTXPN11R	heat shock-induced protein [Homo sapiens] >pir|B45871|B45871 dnaK-type molecular chaperone HSP70-Hom - human >sp|P34931|HS7H_HUMAN HEAT SHOCK 70 KD PROTEIN 1-HOM (HSP70-HOM). Length = 641	gi|188492	3	413	94	98	HTXPN11	Lung, Pancreas, Colon
678	HCDBN37R	heterogeneous nuclear ribonucleoprotein C-like protein - human Length = 328	pir|A44192|A44192	1	300	96	96	HCDBN37	Colon, Breast/Ovarian
679	HABGC02R	HLA-DR-beta-B [Homo sapiens] Length = 266	gi|490048	3	389	89	94	HABGC02	Lung, Colon
680	HNTSA70R	HsMcm6 [Homo sapiens] >sp|Q14566|MCM6_HUMAN DNA REPLICATION LICENSING FACTOR MCM6 (P105MCM). Length = 821	gnl|PID|d1013380	3	341	69	72	HNTSA70	Lung, Colon
681	HDTKP24R	hypothetical 18K protein (rRNA) - goldfish mitochondrion (SGC1) Length = 166	pir|JC1348|JC1348	397	492	64	67	HDTKP24	Lung, Pancreas, Colon
682	HODE114R	hypothetical 18K protein (rRNA) - goldfish mitochondrion (SGC1) Length = 166	pir|JC1348|JC1348	164	247	62	68	HODE114	Lung, Pancreas, Colon
683	HOELC42R	IGF-BP 4 [Homo sapiens] >gnl|PID|e1227579 insulin-like growth factor binding protein 4 [Homo sapiens] >pir|B37252|B37252 insulin-like growth factor-binding protein 4 precursor - human >sp|P22692|IBP4_HUMAN INSULIN-LIKE GROWTH FACTOR BINDING PROTEIN 4 PREC	gi|184816	13	288	83	83	HOELC42	Pancreas, Colon

684	HWAFL44R	immunoglobulin heavy chain [Homo sapiens] >pir|D36005|D36005 Ig heavy chain V region (M43) - human {SUB 38-156} Length = 156	gi|567121	2	463	83	90	HWAFL44	Lung, Colon
685	HABGF46R	immunoglobulin light chain variable region [Homo sapiens] >gi|2970534 (AF049692) immunoglobulin kappa light chain [Homo sapiens] {SUB 3-106} Length = 143	gi|1136555	42	446	71	85	HABGF46	Lung, Pancreas, Colon, Breast/Ovarian
686	HOELC15R	insulin-like growth factor-binding protein [Homo sapiens] >gi|386791 growth factor-binding protein-3 [Homo sapiens] >gi|398164 insulin-like growth factor binding protein 3 [Homo sapiens] >pir|A36578|IOHU3 insulin-like growth factor-binding protein 3 precu	gi|183116	8	424	96	96	HOELC15	Pancreas, Colon, Breast/Ovarian
687	H2LAR26R	keratin 18 [Homo sapiens] >gi|307081 keratin 18 precursor [Homo sapiens] >gi|34037 cytokeratin 18 [Homo sapiens] >pir|S05481|S05481 keratin 18, type I, cytoskeletal - human >sp|P05783|K1CR_HUMAN KERATIN, TYPE I CYTOSKELETAL 18 (CYTOKERATIN 18) (K18) (CK 1	gi|386844	72	476	97	98	H2LAR26	Colon, Breast/Ovarian
688	H2LAV85R	Ku (p70/p80) subunit [Homo sapiens] >gi|307093 Ku antigen [Homo sapiens] >pir|A35051|A32626 Ku antigen 80K chain - human >sp|P13010|KU86_HUMAN ATP-DEPENDENT DNA HELICASE II, 86 KD SUBUNIT (LUPUS KU AUTOANTIGEN PROTEIN P86) (86 KD SUBUNIT OF KU ANTIGEN) (T	gi|307094	67	462	97	98	H2LAV85	Lung, Pancreas
689	HBSDC92R	I-caldesmon II [Homo sapiens] Length = 532	gnl|PID|d1015132	56	337	64	76	HBSDC92	Lung, Breast/Ovarian

690	HUTHN01R	L6 [Homo sapiens] >pir|A42926|A42926 L6 surface protein - human Length = 202	gi|186804	87	545	91	91	HUTHN01	Lung, Pancreas, Colon, Breast/Ovarian
691	H2LAW03R	lactate dehydrogenase B [Homo sapiens] >gi|34329 lactate dehydrogenase B (AA 1 - 334) [Homo sapiens] >pir|S02795|DEHULH L-lactate dehydrogenase (EC 1.1.1.27) chain H - human >sp|P07195|LDHH_HUMAN L-LACTATE DEHYDROGENASE H CHAIN (EC 1.1.1.27) (LDH-B). {SUB	gnl|PID|e223241	111	536	99	100	H2LAW03	Lung, Pancreas
692	HOEMO60R	lactate dehydrogenase-A [Homo sapiens] >gi|34313 lactate dehydrogenase-A [Homo sapiens] >pir|A00347|DEHULM L-lactate dehydrogenase (EC 1.1.1.27) chain M - human >sp|P00338|LDHM_HUMAN L-LACTATE DEHYDROGENASE M CHAIN (EC 1.1.1.27) (LDH-A). {SUB 2-332} Lengt	gi|780261	1	201	59	59	HOEMO60	Pancreas, Breast/Ovarian
693	HKAHJ14R			1	216			HKAHJ14	Pancreas, Colon
694	HOHEA39R	latent transforming growth factor-beta-binding protein - human Length = 1820	pir|A55494|A55494	1	240	85	86	HOHEA39	Pancreas, Breast/Ovarian
695	HOELF72R	lumican [Homo sapiens] Length = 338	gi|699577	58	468	97	97	HOELF72	Pancreas, Colon
696	HAPNX59R	M130 antigen [Homo sapiens] >pir|I38003|S36077 M130 antigen - human >sp|Q07898|Q07898 M130 ANTIGEN PRECURSOR. Length = 1116	gi|312142	1	432	85	88	HAPNX59	Lung, Colon
697	HBJJS17R	methionine aminopeptidase [Homo sapiens] >gi|687243 eIF-2-associated p67 homolog [Homo sapiens] >pir|S52112|DPHUM2 methionyl aminopeptidase (EC 3.4.11.18) 2 - human >sp|P50579|AMP2_HUMAN METHIONINE AMINOPEPTIDASE 2 (EC 3.4.11.18) (METAP 2) (PEPTIDASE M 2)	gi|903982	1	255	100	100	HBJJS17	Lung, Pancreas

698	HATDU61R	midkine [Homo sapiens] >gi|188571 retinoic acid inducible factor [Homo sapiens] >gi|35087 neurite outgrowth-promoting protein [Homo sapiens] >gnl|PID|d1001932 midkine [Homo sapiens] >pir|JH0385|JH0385 midkine precursor - human >sp|P21741|MK_HUMAN MIDKINE	gi|182651	1	108	67	67	HATDU61	Pancreas, Colon
699	HCWHT65R	mitochondrial intermediate peptidase precursor [Homo sapiens] >sp|Q99797|Q99797 MITOCHONDRIAL INTERMEDIATE PEPTIDASE PRECURSOR (EC 3.4.24.59). Length = 713	gi|1763642	1	432	74	77	HCWHT65	Prostate, Colon
700	H2CBN02R	mitochondrial matrix protein [Homo sapiens] >pir|A32800|A32800 chaperonin GroEL precursor - human >sp|P10809|P60_HUMAN MITOCHONDRIAL MATRIX PROTEIN P1 PRECURSOR (P60 LYMPHOCYTE PROTEIN) (60 KD CHAPERONIN) (HEAT SHOCK PROTEIN 60) (HSP-60) (PROTEIN CPN60) (	gi|190127	1	435	99	99	H2CBN02	Pancreas, Colon
701	H2CBV68R	mitochondrial matrix protein [Homo sapiens] >pir|A32800|A32800 chaperonin GroEL precursor - human >sp|P10809|P60_HUMAN MITOCHONDRIAL MATRIX PROTEIN P1 PRECURSOR (P60 LYMPHOCYTE PROTEIN) (60 KD CHAPERONIN) (HEAT SHOCK PROTEIN 60) (HSP-60) (PROTEIN CPN60) (	gi|190127	2	406	100	100	H2CBV68	Colon, Breast/Ovarian

702	H6EDK07R	Mr 110,000 antigen [Homo sapiens] >pir|I52703|I52703 42K membrane glycoprotein - human >sp|Q16186|G100_HUMAN 110 KD CELL MEMBRANE GLYCOPROTEIN. Length = 407	gnl|PID|d1011683	1	252	90	90	H6EDK07	Lung, Breast/Ovarian
703	HACAH10R	NADH dehydrogenase subunit 2, ND2 [human, brain, Peptide Mitochondrial Partial Mutant, 67 aa] [Homo sapiens] >sp|Q36734|Q36734 NADH DEHYDROGENASE SUBUNIT 2 (FRAGMENT). Length = 67	bbs|75898	1	66	89	96	HACAH10	Lung, Pancreas, Colon
704	HCCMC56R	NADH-UBIQUINONE OXIDOREDUCTASE B18 SUBUNIT (EC 1.6.5.3) (EC 1.6.99.3) (COMPLEX I-B18) (CI-B18) (CELL ADHESION PROTEIN SQM1). Length = 134	sp|P17568|NB8M_HUMAN	16	351	83	83	HCCMC56	Lung, Colon, Breast/Ovarian
705	H2CBN54R	NADH-ubiquinone oxidoreductase B22 subunit {C-terminal} [human, placenta, Peptide Mitochondrial Partial, 179 aa] [Homo sapiens] Length = 179	bbs|178894	2	427	99	99	H2CBN54	Pancreas, Colon
706	HMCGL12R	NMB gene product [Homo sapiens] >pir|I38065|I38065 gene NMB protein - human >sp|Q14956|NMB_HUMAN PUTATIVE TRANSMEMBRANE PROTEIN NMB PRECURSOR. Length = 560	gi|666043	96	389	76	80	HMCGL12	Lung, Pancreas
707	HWHPX50R	nucleolar protein [Mus musculus] >pir|I52858|I52858 nucleolar protein - mouse >sp|Q61937|NPM_MOUSE NUCLEOPHOSMIN (NPM) (NUCLEOLAR PHOSPHOPROTEIN B23) (NUMATRIN) (NUCLEOLAR PROTEIN NO38). Length = 292	gi|200011	1	414	87	87	HWHPX50	Lung, Pancreas, Colon, Breast/Ovarian

708	HAPQD84R			115	267			HAPQD84	Lung, Pancreas. Colon, Breast/Ovarian
709	HLIBN66R			1	219			HLIBN66	Lung, Pancreas
710	HE2BD84R	OSF-2p1 [Homo sapiens] >pir|S36111|S36111 osteoblast-specific factor 2 - human >sp|Q15064|Q15064 OSF-2P1. Length = 779	gnl|PID|d1003341	2	394	77	81	HE2BD84	Pancreas, Colon. Breast/Ovarian
711	HLQFY45R	pancreatitis-associated protein [Homo sapiens] >gi|312807 preprotein [Homo sapiens] >bbs|121222 PAP-H=pancreatitis-associated protein [human, pancreas, Peptide, 175 aa] [Homo sapiens] >gnl|PID|d1003233 PAP homologous protein [Homo sapiens] >pir|A49616|A49	gi|482909	57	374	60	66	HLQFY45	Pancreas, Colon
712	HAMGQ78R	phosphate carrier isoform A (alternatively spliced, exon IIIA) - human >sp|Q00325|MPCP_HUMAN MITOCHONDRIAL PHOSPHATE CARRIER PROTEIN PRECURSOR. Length = 362	pir|A53737|A53737	2	352	82	82	HAMGQ78	Lung, Colon
713	HODEV64R	poly(A)-binding protein [Homo sapiens] >gi|1562511 poly(A)-binding protein [Homo sapiens] >sp|P11940|PAB1_HUMAN POLYADENYLATE-BINDING PROTEIN 1 (POLY(A) BINDING PROTEIN 1) (PABP 1). Length = 636	gi|1562511	1	492	97	98	HODEV64	Lung, Pancreas

714	H2CBD48R	precursor polypeptide (AA -21 to 782) [Homo sapiens] >pir|A35954|A35954 endoplasmin precursor - human >sp|P14625|ENPL_HUMAN ENDOPLASMIN PRECURSOR (94 KD GLUCOSE-REGULATED PROTEIN) (GRP94) (GP96 HOMOLOG) (TUMOR REJECTION ANTIGEN 1). Length = 803	gi|37261	2	499	95	97	H2CBD48	Pancreas, Colon
715	HCCMA82R	procarboxypeptidase B [Homo sapiens] >pir|A42332|A42332 carboxypeptidase B (EC 3.4.17.2) precursor, pancreatic - human Length = 416	gi|189625	3	383	94	94	HCCMA82	Pancreas, Colon
716	HOEMK78R	prostacyclin-stimulating factor, PGI2-stimulating factor, PSF [human, cultured diploid fibroblast cells, Peptide, 282 aa] [Homo sapiens] >pir|S50031|S50031 prostacyclin-stimulating factor - human >sp|Q16270|Q16270 PROSTACYCLIN-STIMULATING FACTOR. Length =	bbs|161346	3	329	95	95	HOEMK78	Lung, Pancreas
717	H2CBD13R	proteasome subunit C9 [Homo sapiens] >pir|S15972|SNHUC9 multicatalytic endopeptidase complex (EC 3.4.99.46) chain C9 - human >sp|P25789|PRC9_HUMAN PROTEASOME COMPONENT C9 (EC 3.4.99.46) (MACROPAIN SUBUNIT C9) (MULTICATALYTIC ENDOPEPTIDASE COMPLEX SUBUNIT	gnl|PID|d1001118	156	461	100	100	H2CBD13	Lung, Pancreas, Prostate, Colon, Breast/Ovarian
718	HCFMU61R	protein-tyrosine kinase (EC 2.7.1.112) ZAP-70 - human Length = 619	pir|A44266|A44266	1	477	98	98	HCFMU61	Pancreas, Colon

719	HOSNE94R	proteoglycan core protein [Homo sapiens] >pir|A45016|NBHUC8 decorin precursor - human >sp|P07585|PGS2_HUMAN BONE PROTEOGLYCAN II PRECURSOR (PG-S2) (DECORIN) (PG40). >gi|1161226 decorin [Rattus norvegicus] {SUB 204-299} Length = 359	gi|181170	2	466	85	85	HOSNE94	Lung, Pancreas
720	HCROZ08R	putative precursor (AA 1-304) [Homo sapiens] >gnl|PID|e224276 uracil-DNA-glycosylase, UNG1 [Homo sapiens] >pir|S05964|A60472 uracil-DNA glycosylase (EC 3.-.-.-) precursor - human >gnl|PID|e1296296 MITOCHONDRIAL LOCALIZATION PEPTIDE [unidentified] {SUB 1-3	gi|37599	3	218	100	100	HCROZ08	Lung, Pancreas, Colon
721	HHBEF47R	pyruvate dehydrogenase E1-alpha precursor [Homo sapiens] >pir|A60225|A60225 pyruvate dehydrogenase (lipoamide) (EC 1.2.4.1) alpha chain - bovine (fragment) {SUB 54-74} Length = 414	gi|387011	1	330	88	88	HHBEF47	Colon, Breast/Ovarian
722	HTXPI31R	pyruvate kinase M2 [Sus scrofa] >sp|Q29582|Q29582 PYRUVATE KINASE M2 (EC 2.7.1.40) (PHOSPHOENOLPYRUVATE KINASE) (PHOSPHOENOL TRANSPHOSPHORYLASE) (FRAGMENT). Length = 108	gi|972104	2	286	84	85	HTXPI31	Pancreas, Breast/Ovarian
723	HOEKC30R	rhoC coding region (AA 1-193) [Homo sapiens] >gi|407699 GTPase [Homo sapiens] >pir|S01029|TVHURC GTP-binding protein rhoC - human Length = 193	gi|36034	2	151	94	94	HOEKC30	Lung, Pancreas, Breast/Ovarian
724	HOSNR67R	ribosmal protein small subunit [Homo sapiens] Length = 264	gi|306553	1	483	97	98	HOSNR67	Lung, Pancreas

725	H2LAV92R	ribosomal protein [Homo sapiens] >gi|57078 ribosomal protein L38 [Rattus rattus] >pir|S15658|R5RT38 ribosomal protein L38 - rat >pir|S38385|S38385 ribosomal protein L38 - human >gnl|PID|d1026783 (AB007185) ribosomal protein L38 [Homo sapiens] {SUB 34-70}	gi|407423	13	351	72	72	H2LAV92	Lung, Pancreas, Prostate, Colon, Breast/Ovarian
726	H2LAO74R	ribosomal protein L10 [Homo sapiens] >sp|D1026771|D1026771 RIBOSOMAL PROTEIN L15 (FRAGMENT). {SUB 16-57} Length = 205	gi|414587	359	502	83	83	H2LAO74	Lung, Pancreas, Colon, Breast/Ovarian
727	HKMMF85R	ribosomal protein L18a [Homo sapiens] >gi|3702270 (AC005796) ribosomal protein L18a [Homo sapiens] >gnl|PID|d1029536 (AB007175) ribosomal protein L18a [Homo sapiens] {SUB 111-176} Length = 176	gi|401845	1	360	96	96	HKMMF85	Lung, Breast/Ovarian
728	HCLBZ27R	ribosomal protein L19 [Homo sapiens] >bbs|127872 ribosomal protein L19 [human, breast cancer cell line, MCF-7, Peptide, 196 aa] [Homo sapiens] >gi|206726 ribosomal protein L19 [Rattus norvegicus] >gnl|PID|e218038 ribosomal protein L19 [Rattus norvegicus]	gi|36128	19	273	93	98	HCLBZ27	Lung, Pancreas, Colon
729	H2LAV11R	ribosomal protein L21 [Homo sapiens] >gi|984143 ribosomal protein L21 [Homo sapiens] >pir|S55913|S55913 ribosomal protein L21, cytosolic - human >sp|D1026774|D1026774 RIBOSOMAL PROTEIN L21 (FRAGMENT). {SUB 124-154} Length = 160	gi|550015	126	530	99	99	H2LAV11	Lung, Pancreas, Colon

730	HBAGP60R	ribosomal protein L27 [Homo sapiens] >gi|3115335 ribosomal protein L27 [Homo sapiens] >gi|57694 ribosomal protein L27 (AA 1 - 136) [Rattus norvegicus] >gi|62981 ribosomal protein L27 [Gallus gallus] >pir|S00401|R5RT27 ribosomal protein L27, cytosolic - ra	gi|388769	161	373	66	70	HBAGP60	Pancreas, Colon
731	HOEMJ56R	ribosomal protein L28 [Homo sapiens] >pir|S55915|S55915 ribosomal protein L28 - human Length = 137	gi|550019	3	206	94	94	HOEMJ56	Lung, Colon, Breast/Ovarian
732	HA5AF77R	ribosomal protein L31 [Sus scrofa] >gi|36130 ribosomal protein L31 (AA 1-125) [Homo sapiens] >gi|57115 ribosomal protein L31 (AA 1-125) [Rattus norvegicus] >pir|S05576|R5HU31 ribosomal protein L31 - human >pir|A26417|R5RT31 ribosomal protein L31 - rat >gn	gnl|PID|e276436	1	381	82	82	HA5AF77	Lung, Prostate, Colon, Breast/Ovarian
733	H2MAC95R	ribosomal protein L37 [Homo sapiens] >bbs|172744 ribosomal protein L37 {C2-C2 zinc-finger-like} [human, HeLa cells, Peptide, 97 aa] [Homo sapiens] >gnl|PID|d1005426 ribosomal protein L37 [Homo sapiens] >gi|57121 ribosomal protein L37 [Rattus norvegicus] >	gi|292441	67	411	79	79	H2MAC95	Lung, Colon, Breast/Ovarian
734	HDPLP40R	ribosomal protein L37 [Homo sapiens] >bbs|172744 ribosomal protein L37 {C2-C2 zinc-finger-like} [human, HeLa cells, Peptide, 97 aa] [Homo sapiens] >gnl|PID|d1005426 ribosomal protein L37 [Homo sapiens] >gi|57121 ribosomal protein L37 [Rattus norvegicus] >	gi|292441	1	363	100	100	HDPLP40	Lung, Pancreas, Breast/Ovarian

735	HOEMK92R	ribosomal protein L37a [Homo sapiens] >gi|36134 ribosomal protein L37a [Homo sapiens] >gi|57123 ribosomal protein L37a (AA 1 - 92) [Rattus rattus] >gi|312414 ribosomal protein L37a [Mus musculus] >pir|S05014|R5RT37 ribosomal protein L37a - rat >pir|S42109	gi|292439	3	185	96	96	HOEMK92	Lung, Pancreas, Breast/Ovarian
736	HABAD57R	ribosomal protein L4 [Homo sapiens] >pir|S39803|S39803 ribosomal protein L4 - human Length = 425	gi|307385	210	431	80	90	HABAD57	Lung, Pancreas
737	HLXNA52R	ribosomal protein L4 [Rattus norvegicus] Length = 421	gnl|PID|e121603	3	296	86	86	HLXNA52	Lung, Pancreas
738	HWAFK82R	ribosomal protein L9 [Homo sapiens] >gnl|PID|d1003911 'human homologue of rat ribosomal protein L9' [Homo sapiens] Length = 192	gi|710366	139	354	77	78	HWAFK82	Lung, Colon, Breast/Ovarian
739	H2CBL68R	ribosomal protein S13 [Homo sapiens] >gi|488417 ribosomal protein S13 [Homo sapiens] >gnl|PID|d1014222 ribosomal protein S13 [Homo sapiens] >gi|57730 ribosomal protein S13 [Rattus rattus] >pir|S34109|S34109 ribosomal protein S13, cytosolic - human >pir|A3	gi|307391	3	461	100	100	H2CBL68	Lung, Pancreas
740	HNTNE17R	ribosomal protein S17 [Homo sapiens] >gi|337503 S17 ribosomal protein [Homo sapiens] >pir|JT0405|R4HU17 ribosomal protein S17, cytosolic - human Length = 135	gi|337501	1	387	100	100	HNTNE17	Lung, Pancreas, Breast/Ovarian
741	HBJLR37R	ribosomal protein S26 [Homo sapiens] Length = 115	gi|296452	2	328	98	100	HBJLR37	Pancreas, Colon, Breast/Ovarian

742	HOSNG20R	ribosomal protein S4X isoform [Homo sapiens] >gi|2791861 (AF041428) ribosomal protein s4 X isoform [Homo sapiens] >gi|200864 ribosomal protein S4 [Mus musculus] >gi|57135 ribosomal protein S4 (AA 1 - 263) [Rattus rattus] >gnl|PID|d1002335 ribosomal protei	gi|337510	1	357	97	98	HOSNG20	Lung, Pancreas, Colon, Breast/Ovarian
743	HCLBZ30R	ribosomal protein S5 [Mus musculus] Length = 204	gi|1685071	2	244	89	89	HCLBZ30	Lung, Pancreas, Colon, Breast/Ovarian
744	HBGNY11R	ribosomal protein S8 [Homo sapiens] >gi|57139 ribosomal protein S8 (AA 1-208) [Rattus norvegicus] >gi|313298 ribosomal protein S8 [Mus musculus] >pir|S01609|R3RT8 ribosomal protein S8 - rat >pir|S42110|S42110 ribosomal protein S8 - mouse >pir|S25022|S2502	gi|36150	2	334	100	100	HBGNY11	Lung, Pancreas, Breast/Ovarian
745	HOEKC80R	S19 ribosomal protein [Homo sapiens] >pir|I52692|I52692 ribosomal protein S19, cytosolic - human Length = 145	gi|337733	2	376	98	98	HOEKC80	Lung, Pancreas, Colon, Breast/Ovarian
746	HCHBM70R	secretory protein [Homo sapiens] >gi|940946 intestinal trefoil factor [Homo sapiens] >pir|A48284|A48284 intestinal trefoil factor 3 precursor - human >sp|Q07654|ITF_HUMAN INTESTINAL TREFOIL FACTOR PRECURSOR (HP1.B). Length = 80	gi|402483	1	114	57	57	HCHBM70	Colon, Breast/Ovarian
747	HFCES53R	semaphorin C [Mus musculus] >pir|I48746|I48746 semaphorin C - mouse (fragment) >sp|Q62179|Q62179 SEMAPHORIN C (SEM C) (FRAGMENT). Length = 782	gi|854328	1	165	80	86	HFCES53	Colon, Breast/Ovarian

748	HCRQC92R	spermidine/spermine N1-acetyltransferase [Homo sapiens] >gi|338336 spermidine/spermine N1-acetyltransferase [Homo sapiens] >sp|P21673|ATDA_HUMAN DIAMINE ACETYLTRANSFERASE (EC 2.3.1.57) (SPERMIDINE/SPERMINE N1-ACETYLTRANSFERASE) (SSAT) (PUTRESCINE ACETYLT	gi|338392	3	278	98	98	HCRQC92	Lung. Colon. Breast/Ovarian
749	HAOAG75R	TARBP-b gene product [Homo sapiens] Length = 277	gi|347964	2	418	100	100	HAOAG75	Lung. Colon
750	HWAFE36R	TEGT gene product [Homo sapiens] >pir|I38334|I38334 TEGT (testis enhanced gene transcript) - human Length = 237	gi|458545	2	127	100	100	HWAFE36	Pancreas, Colon
751	HBGOU57R	TIMP gene product [Homo sapiens] >gi|182483 prefibroblast collagenase inhibitor [Homo sapiens] >gi|189382 collagenase inhibitor [Homo sapiens] >gi|37183 precursor [Homo sapiens] >pir|A93372|ZYHUEP metalloproteinase tissue inhibitor 1 precursor - human >gi	gi|490094	60	314	75	75	HBGOU57	Lung. Pancreas. Breast/Ovarian
752	HTXPF20R	TIMP gene product [Homo sapiens] >gi|182483 prefibroblast collagenase inhibitor [Homo sapiens] >gi|189382 collagenase inhibitor [Homo sapiens] >gi|37183 precursor [Homo sapiens] >pir|A93372|ZYHUEP metalloproteinase tissue inhibitor 1 precursor - human >gi	gi|490094	1	549	84	84	HTXPF20	Lung. Pancreas. Colon. Breast/Ovarian
753	HCRMD09R	transforming growth factor-beta 1 binding protein precursor [Homo sapiens] >pir|A35626|A35626 transforming growth factor beta-1-binding protein - human Length = 1394	gi|339548	2	460	86	87	HCRMD09	Lung. Pancreas. Colon

754	HAJRB47R	triose-phosphate isomerase [Pan troglodytes] >gi|37247 triosephosphate isomerase [Homo sapiens] >gi|1200507 triosephosphate isomerase [Homo sapiens] >gi|339841 triosephosphate isomerase (EC 5.3.1.1) [Homo sapiens] >pir|S29743|ISHUT triose-phosphate isomer	gi|176960	2	334	100	100	HAJRB47	Lung, Pancreas, Breast/Ovarian
755	HABGB36R			6	251			HABGB36	Lung, Breast/Ovarian
756	HADBF86R			3	158			HADBF86	Lung, Colon
757	HADDP09R			2	97			HADDP09	Lung, Pancreas, Colon, Breast/Ovarian
758	HAGCY06R			2	58			HAGCY06	Pancreas, Breast/Ovarian
759	HAGDI75R			1	66			HAGDI75	Colon, Breast/Ovarian
760	HAHBD47R			118	429			HAHBD47	Lung, Pancreas
761	HAHCR61R			165	422			HAHCR61	Pancreas, Colon
762	HAJAU22R			101	202			HAJAU22	Pancreas, Colon
763	HAMGB62R			212	370			HAMGB62	Lung, Pancreas, Colon, Breast/Ovarian
764	HANGC52R			3	98			HANGC52	Lung, Pancreas, Colon
765	HAPCF30R			2	94			HAPCF30	Lung, Colon
766	HAPPV45R			216	536			HAPPV45	Lung, Pancreas
767	HAPQK19R			200	415			HAPQK19	Lung, Pancreas
768	HAPRL82R			3	233			HAPRL82	Lung, Pancreas
769	HAQBT45R			40	255			HAQBT45	Lung, Colon
770	HAUAL56R			127	315			HAUAL56	Pancreas, Breast/Ovarian

771	HAUBR22R	2	67	HAUBR22	Pancreas, Colon, Breast/Ovarian
772	HBAFN19R	3	257	HBAFN19	Lung, Colon, Breast/Ovarian
773	HBGOK25R	274	528	HBGOK25	Pancreas, Colon
774	HBGRA76R	2	88	HBGRA76	Pancreas, Colon
775	HBGRB47R	1	111	HBGRB47	Lung, Pancreas, Colon, Breast/Ovarian
776	HBJAS24R	1	66	HBJAS24	Colon, Breast/Ovarian
777	HBJKI05R	207	362	HBJKI05	Pancreas, Colon
778	HBKEC86R	254	409	HBKEC86	Pancreas, Colon
779	HBLGD42R	3	341	HBLGD42	Lung, Pancreas, Colon, Breast/Ovarian
780	HBPAF10R	3	65	HBPAF10	Lung, Pancreas
781	HCDBU02R	65	184	HCDBU02	Pancreas, Colon
782	HCDBU04R	64	348	HCDBU04	Lung, Pancreas, Colon
783	HCDDT61R	2	121	HCDDT61	Pancreas, Colon
784	HCEGY65R	2	79	HCEGY65	Pancreas, Colon
785	HCHAK80R	1	513	HCHAK80	Colon, Breast/Ovarian
786	HCHMW79R	73	432	HCHMW79	Pancreas, Breast/Ovarian
787	HCHOB92R	93	350	HCHOB92	Colon, Breast/Ovarian
788	HCLBO01R	45	149	HCLBO01	Lung, Colon
789	HCQAN60R	3	122	HCQAN60	Pancreas, Colon
790	HCRAK70R	3	293	HCRAK70	Colon, Breast/Ovarian
791	HCRPC63R	1	129	HCRPC63	Pancreas, Colon
792	HCUDC51R	2	265	HCUDC51	Lung, Colon

793	HDPFI40R	139	453	HDPFI40	Lung, Pancreas, Breast/Ovarian
794	HDPLP23R	1	141	HDPLP23	Pancreas, Colon, Breast/Ovarian
795	HDPRZ54R	1	165	HDPRZ54	Colon, Breast/Ovarian
796	HE9DP46R	2	166	HE9DP46	Lung, Pancreas, Colon
797	HEGAR19R	361	534	HEGAR19	Lung, Colon
798	HFAUO64R	27	137	HFAUO64	Colon, Breast/Ovarian
799	HFIAL90R	186	308	HFIAL90	Lung, Colon
800	HHBEQ12R	218	514	HHBEQ12	Lung, Pancreas
801	HHEUL94R	2	127	HHEUL94	Lung, Pancreas, Colon
802	HISCF76R	16	153	HISCF76	Pancreas, Colon
803	HJMAU64R	1	207	HJMAU64	Lung, Colon
804	HJPCI25R	275	508	HJPCI25	Lung, Pancreas, Colon
805	HKBAC48R	369	542	HKBAC48	Lung, Pancreas, Colon, Breast/Ovarian
806	HKBAD57R	165	341	HKBAD57	Lung, Pancreas
807	HKDBA91R	3	332	HKDBA91	Pancreas, Colon
808	HKGDB80R	3	224	HKGDB80	Lung, Colon
809	HLDNC95R	289	537	HLDNC95	Lung, Pancreas, Prostate, Colon
810	HMSNI52R	2	271	HMSNI52	Lung, Pancreas
811	HODAY16R	134	298	HODAY16	Colon, Breast/Ovarian
812	HODEA57R	289	471	HODEA57	Lung, Pancreas
813	HOEMO27R	1	60	HOEMO27	Colon, Breast/Ovarian

814	HOEMO62R	2	73	HOEMO62	Pancreas, Breast/Ovarian
815	HOEMS18R	1	102	HOEMS18	Lung, Pancreas, Colon, Breast/Ovarian
816	HOENU53R	115	267	HOENU53	Lung, Colon
817	HOGAP33R	1	498	HOGAP33	Pancreas, Prostate, Breast/Ovarian
818	HOSMV34R	124	327	HOSMV34	Lung, Pancreas, Breast/Ovarian
819	HOSNF25R	405	587	HOSNF25	Pancreas, Colon
820	HOUHO32R	230	391	HOUHO32	Lung, Colon
821	HP1AC23R	2	286	HP1AC23	Lung, Breast/Ovarian
822	HRAAD31R	115	414	HRAAD31	Lung, Colon
823	HRACR12R	2	100	HRACR12	Pancreas, Colon
824	HRADJ57R	2	142	HRADJ57	Lung, Colon
825	HROAX48R	184	285	HROAX48	Pancreas, Colon
826	HTAHR87R	369	491	HTAHR87	Lung, Pancreas
827	HTTIO45R	1	288	HTTIO45	Colon, Breast/Ovarian
828	HTWDH05R	1	420	HTWDH05	Lung, Pancreas, Colon, Breast/Ovarian
829	HUFDS13R	51	152	HUFDS13	Pancreas, Colon
830	HUSZE86R	2	340	HUSZE86	Pancreas, Colon
831	HUTHF75R	161	418	HUTHF75	Lung, Pancreas, Breast/Ovarian
832	HWAFW07R	3	170	HWAFW07	Lung, Pancreas, Colon
833	HWLIB82R	209	403	HWLIB82	Pancreas, Colon
834	HWLLX91R	147	302	HWLLX91	Lung, Colon
835	HWLMZ54R	1	120	HWLMZ54	Pancreas, Colon

836	HMIAI78R			173	319			HMIAI78	Pancreas, Colon, Breast/Ovarian
837	HBGFJ39R	unknown product specific to adipose tissue [Homo sapiens] >sp|Q15847|Q15847 HYPOTHETICAL 7.9 KD PROTEIN. Length = 76	gnl|PID|d1008821	1	153	100	100	HBGFJ39	Pancreas, Colon
838	HAMHH32R			1	123			HAMHH32	Lung, Colon
839	HAQBQ95R			104	205			HAQBQ95	Colon, Breast/Ovarian
840	HAGHY58R	URF 1 (NADH dehydrogenase subunit) [Homo sapiens] >gi|337189 protein 1 [Homo sapiens] >pir|A00407|DNHUN1 NADH dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 1 - human mitochondrion (SGC1) >sp|P03886|NU1M_HUMAN NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 1 (EC 1.6	gi|13004	157	411	95	95	HAGHY58	Lung, Colon
841	HOSNE37R	URF 2 (NADH dehydrogenase subunit) [Homo sapiens] >gi|2052363 protein 2 [Homo sapiens] >gi|2582057 (AF014882) NADH dehydrogenase subunit 2 [Homo sapiens] >gi|2582061 (AF014884) NADH dehydrogenase subunit 2 [Homo sapiens] >gi|2582063 (AF014885) NADH dehydr	gi|578710	73	231	59	62	HOSNE37	Lung, Pancreas, Colon
842	HWAFE41R	VDUP1=1,25-dihydroxyvitamin D-3 up-regulated [human, HL-60 promyelocytic leukemia cells, Peptide, 391 aa] [Homo sapiens] Length = 391	bbs|155932	2	508	84	84	HWAFE41	Pancreas, Colon

The first column of Table 1 shows the "SEQ ID NO:" for each of the 842 cancer antigen polynucleotide sequences of the invention.

The second column in Table 1, provides a unique "Sequence/Contig ID" identification for each cancer associated sequence. The third column in Table 1, "Gene Name," provides a putative identification of the gene based on the sequence similarity of its translation product to an amino acid sequence found in a publicly accessible gene database, such as GenBank (NCBI). The great majority of the cDNA sequences reported in Table 1 are unrelated to any sequences previously described in the literature. The fourth column, in Table 1, "Overlap," provides the database accession no. for the database sequence having similarity. The fifth and sixth columns in Table 1 provide the location (nucleotide position nos. within the contig), "Start" and "End", in the polynucleotide sequence "SEQ ID NO:X" that delineate the preferred ORF shown in the sequence listing as SEQ ID NO:Y. In one embodiment, the invention provides a protein comprising, or alternatively consisting of, a polypeptide encoded by the portion of SEQ ID NO:X delineated by the nucleotide position nos. "Start" and "End". Also provided are polynucleotides encoding such proteins and the complementary strand thereto. The seventh and eighth columns provide the "% Identity" (percent identity) and "% Similarity" (percent similarity) observed between the aligned sequence segments of the translation product of SEQ ID NO:X and the database sequence.

The ninth column of Table 1 provides a unique "Clone ID" for a clone related to each contig sequence. This clone ID references the cDNA clone which contains at least the 5' most sequence of the assembled contig and at least a portion of SEQ ID NO:X was determined by directly sequencing the referenced clone. The reference clone may have more sequence than described in the sequence listing or the clone may have less. In the vast majority of cases, however, the clone is believed to encode a full-length polypeptide. In the case where a clone is not full-length, a full-length cDNA can be obtained by methods described elsewhere herein.

The tenth column of Table 1, "Tissue," provides the tissue source where each unique SEQ ID NO:X was found to be predominantly expressed.

Table 3 indicates public ESTs, of which at least one, two, three, four, five, ten, or more of any one or more of these public ESTs are optionally excluded from the invention.

SEQ ID NO:X (where X may be any of the polynucleotide sequences disclosed in the sequence listing as SEQ ID NO:1 through SEQ ID NO:842) and the translated SEQ ID NO:Y

(where Y may be any of the polypeptide sequences disclosed in the sequence listing as SEQ ID NO:843 through SEQ ID NO:1684) are sufficiently accurate and otherwise suitable for a variety of uses well known in the art and decribed further below. For instance, SEQ ID NO:X has uses including, but not limited to, in designing nucleic acid hybridization probes that will detect nucleic acid sequences contained in SEQ ID NO:X or the related cDNA clone contained in a library deposited with the ATCC. These probes will also hybridize to nucleic acid molecules in biological samples, thereby enabling immediate applications in chromosome mapping, linkage analysis, tissue identification and/or typing, and a variety of forensic and diagnostic methods of the invention. Similarly, polypeptides identified from SEQ ID NO:Y have uses that include, but are not limited to, generating antibodies which bind specifically to the cancer antigen polypeptides, or fragments thereof, and/or to the cancer antigen polypeptides encoded by the cDNA clones identified in Table 1.

Nevertheless, DNA sequences generated by sequencing reactions can contain sequencing errors. The errors exist as misidentified nucleotides, or as insertions or deletions of nucleotides in the generated DNA sequence. The erroneously inserted or deleted nucleotides cause frame shifts in the reading frames of the predicted amino acid sequence. In these cases, the predicted amino acid sequence diverges from the actual amino acid sequence, even though the generated DNA sequence may be greater than 99.9% identical to the actual DNA sequence (for example, one base insertion or deletion in an open reading frame of over 1000 bases).

Accordingly, for those applications requiring precision in the nucleotide sequence or the amino acid sequence, the present invention provides not only the generated nucleotide sequence identified as SEQ ID NO:X, the predicted translated amino acid sequence identified as SEQ ID NO:Y, but also a sample of plasmid DNA containing the related cDNA clone (deposited with the ATCC, as set forth in Table 1). The nucleotide sequence of each deposited clone can readily be determined by sequencing the deposited clone in accordance with known methods. Further, techniques known in the art can be used to verify the nucleotide sequences of SEQ ID NO:X.

The predicted amino acid sequence can then be verified from such deposits. Moreover, the amino acid sequence of the protein encoded by a particular clone can also be directly determined by peptide sequencing or by expressing the protein in a suitable host cell containing the deposited human cDNA, collecting the protein, and determining its sequence.

The present invention also relates to vectors or plasmids which include such DNA sequences, as well as the use of the DNA sequences. The material deposited with the ATCC on:

Table 2

ATCC Deposits	Deposit Date	ATCC Designation Number
LP01, LP02, LP03, LP04, LP05, LP06, LP07, LP08, LP09, LP10, LP11,	May-20-97	209059, 209060, 209061, 209062, 209063, 209064, 209065, 209066, 209067, 209068, 209069
LP12	Jan-12-98	209579
LP13	Jan-12-98	209578
LP14	Jul-16-98	203067
LP15	Jul-16-98	203068
LP16	Feb-1-99	203609
LP17	Feb-1-99	203610
LP20	Nov-17-98	203485
LP21	Jun-18-99	PTA-252
LP22	Jun-18-99	PTA-253
LP23	Dec-22-99	PTA-1081

each is a mixture of cDNA clones derived from a variety of human tissue and cloned in either a plasmid vector or a phage vector, as shown in Table 5. These deposits are referred to as "the deposits" herein. The tissues from which the clones were derived are listed in Table 5, and the vector in which the cDNA is contained is also indicated in Table 5. The deposited material includes the cDNA clones which were partially sequenced and are related to the SEQ ID NO:X described in Table 1 (column 9). Thus, a clone which is isolatable from the ATCC Deposits by use of a sequence listed as SEQ ID NO:X may include the entire coding region of a human gene or in other cases such clone may include a substantial portion of the coding region of a human gene. Although the sequence listing lists only a portion of the DNA sequence in a clone included in the ATCC Deposits, it is well within the ability of one skilled in the art to complete the sequence of the DNA included in a clone isolatable from the

ATCC Deposits by use of a sequence (or portion thereof) listed in Table 1 by procedures hereinafter further described, and others apparent to those skilled in the art.

Also provided in Table 5 is the name of the vector which contains the cDNA clone. Each vector is routinely used in the art. The following additional information is provided for convenience.

Vectors Lambda Zap (U.S. Patent Nos. 5,128,256 and 5,286,636), Uni-Zap XR (U.S. Patent Nos. 5,128, 256 and 5,286,636), Zap Express (U.S. Patent Nos. 5,128,256 and 5,286,636), pBluescript (pBS) (Short, J. M. et al., *Nucleic Acids Res. 16:*7583-7600 (1988); Alting-Mees, M. A. and Short, J. M., *Nucleic Acids Res. 17:*9494 (1989)) and pBK (Alting-Mees, M. A. et al., *Strategies 5:*58-61 (1992)) are commercially available from Stratagene Cloning Systems, Inc., 11011 N. Torrey Pines Road, La Jolla, CA, 92037. pBS contains an ampicillin resistance gene and pBK contains a neomycin resistance gene. Phagemid pBS may be excised from the Lambda Zap and Uni-Zap XR vectors, and phagemid pBK may be excised from the Zap Express vector. Both phagemids may be transformed into *E. coli* strain XL-1 Blue, also available from Stratagene.

Vectors pSport1, pCMVSport 1.0, pCMVSport 2.0 and pCMVSport 3.0, were obtained from Life Technologies, Inc., P. O. Box 6009, Gaithersburg, MD 20897. All Sport vectors contain an ampicillin resistance gene and may be transformed into *E. coli* strain DH10B, also available from Life Technologies. See, for instance, Gruber, C. E., et al., *Focus 15:*59 (1993). Vector lafmid BA (Bento Soares, Columbia University, New York, NY) contains an ampicillin resistance gene and can be transformed into *E. coli* strain XL-1 Blue. Vector pCR®2.1, which is available from Invitrogen, 1600 Faraday Avenue, Carlsbad, CA 92008, contains an ampicillin resistance gene and may be transformed into *E. coli* strain DH10B, available from Life Technologies. See, for instance, Clark, J. M., *Nuc. Acids Res. 16:*9677-9686 (1988) and Mead, D. *et al., Bio/Technology 9:* (1991).

The present invention also relates to the genes corresponding to SEQ ID NO:X, SEQ ID NO:Y, and/or the cDNA contained in a deposited cDNA clone. The corresponding gene can be isolated in accordance with known methods using the sequence information disclosed herein. Such methods include, but are not limited to, preparing probes or primers from the disclosed sequence and identifying or amplifying the corresponding gene from appropriate sources of genomic material.

Also provided in the present invention are allelic variants, orthologs, and/or species homologs. Procedures known in the art can be used to obtain full-length genes, allelic variants, splice variants, full-length coding portions, orthologs, and/or species homologs of genes corresponding to SEQ ID NO:X, SEQ ID NO:Y, and/or the cDNA contained in the related cDNA clone in the deposit, using information from the sequences disclosed herein or the clones deposited with the ATCC. For example, allelic variants and/or species homologs may be isolated and identified by making suitable probes or primers from the sequences provided herein and screening a suitable nucleic acid source for allelic variants and/or the desired homologue.

The present invention provides a polynucleotide comprising, or alternatively consisting of, the nucleic acid sequence of SEQ ID NO:X, and/or the related cDNA clone (See, e.g., columns 1 and 9 of Table 1). The present invention also provides a polypeptide comprising, or alternatively, consisting of, the polypeptide sequence of SEQ ID NO:Y, a polypeptide encoded by SEQ ID NO:X, and/or a polypeptide encoded by the cDNA in the related cDNA clone contained in a deposited library. Polynucleotides encoding a polypeptide comprising, or alternatively consisting of, the polypeptide sequence of SEQ ID NO:Y, a polypeptide encoded by SEQ ID NO:X, and/or a polypeptide encoded by the the dDNA in the related cDNA clone contained in a deposited library, are also encompassed by the invention. The present invention further encompasses a polynucleotide comprising, or alternatively consisting of, the complement of the nucleic acid sequence of SEQ ID NO:X, and/or the complement of the coding strand of the related cDNA clone contained in a deposited library.

Many polynucleotide sequences, such as EST sequences, are publicly available and accessible through sequence databases and may have been publicly available prior to conception of the present invention. Preferably, such related polynucleotides are specifically excluded from the scope of the present invention. To list every related sequence would unduly burden the disclosure of this application. Accordingly, for each "Contig Id" listed in the first column of Table 3, preferably excluded are one or more polynucleotides comprising a nucleotide sequence described in the second column of Table 3 by the general formula of a-b, each of which are uniquely defined for the SEQ ID NO:X corresponding to that Contig Id in Table 1. Additionally, specific embodiments are directed to polynucleotide sequences excluding at least one, two, three, four, five, ten, or more of the specific polynucleotide sequences referenced by the Genbank Accession No. for each Contig Id which may be

included in column 3 of Table 3. In no way is this listing meant to encompass all of the sequences which may be excluded by the general formula, it is just a representative example.

Table 3.

Sequence/ Contig ID	General formula	Genbank Accession No.
507291	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 542 of SEQ ID NO:1, b is an integer of 15 to 556, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:1, and where b is greater than or equal to a + 14.	
508000	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 2648 of SEQ ID NO:2, b is an integer of 15 to 2662, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:2, and where b is greater than or equal to a + 14.	T40333, T41194, T66286, T66339, T73997, T86453, T87207, R17614, R19835, R43336, R45934, R48920, R53521, R43336, R45934, R61813, R75928, R75937, H30115, H42959, H39114, H43825, AA028010, AA028107, AA028148, AA031964, AA032046, AA035668, AA190570, AA233781, AA461489, AA460726, AA460898
518325	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 324 of SEQ ID NO:3, b is an integer of 15 to 338, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:3, and where b is greater than or equal to a + 14.	
523111	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 799 of SEQ ID NO:4, b is an integer of 15 to 813, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:4, and where b is greater than or equal to a + 14.	
526869	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 887 of SEQ ID NO:5, b is an integer of 15 to 901, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:5, and where b is greater than or equal to a + 14.	AA459771
532211	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 717 of SEQ ID NO:6, b is an integer of 15 to 731, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:6, and where b is greater than or equal to a + 14.	H30209, H92182, W95693, W95692, AA196967
532247	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b,	R14583, R93797, H52942, H75493, H78857, W17094, W38705, W81551, W90159, N90874, AA010244,

	where a is any integer between 1 to 2760 of SEQ ID NO:7, b is an integer of 15 to 2774, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:7, and where b is greater than or equal to a + 14.	AA029093, AA126501, AA147066
537932	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 2599 of SEQ ID NO:8, b is an integer of 15 to 2613, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:8, and where b is greater than or equal to a + 14.	T91131, T84801, T85952, R59198, R59256, H43456, H59480, H79111, N26560, N35676, N64506, N66078, N76033, N78705, W07594, W70111, W70169, N90844, AA026910, AA026911, AA057689, AA079631, AA079805, AA131257, AA136081, AA165115, AA210764, AA211886, AA232838, AA262352
540117	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1087 of SEQ ID NO:9, b is an integer of 15 to 1101, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:9, and where b is greater than or equal to a + 14.	T49371, T49372, T49850, T61568, T64892, N39534, W57682, AA031859
547710	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1359 of SEQ ID NO:10, b is an integer of 15 to 1373, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:10, and where b is greater than or equal to a + 14.	R11154, R11155, R61204, R61205, R82674, H06105, R88575, R88638, H89977, H97031, N20224, W01143, W39387, W90318, W90788, AA001027, AA045864, AA045839, AA070190, AA070357, AA070481, AA074270, AA099007, AA099084, AA100370, AA112324, AA113319, AA158425, AA161510, AA171909, AA172133, AA173087, AA181768, AA188815, AA188874, AA190370, AA226831, AA252143
551747	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 3790 of SEQ ID NO:11, b is an integer of 15 to 3804, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:11, and where b is greater than or equal to a + 14.	
552799	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 2143 of SEQ ID NO:12, b is an integer of 15 to 2157, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:12, and where b is greater than or equal to a + 14.	
553243	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1103 of SEQ ID NO:13, b is an integer of 15 to 1117, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:13, and where b is	H63183, W61352, AA151059

	greater than or equal to a + 14.	
553368	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 871 of SEQ ID NO:14, b is an integer of 15 to 885, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:14, and where b is greater than or equal to a + 14.	
554349	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1010 of SEQ ID NO:15, b is an integer of 15 to 1024, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:15, and where b is greater than or equal to a + 14.	
558491	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 531 of SEQ ID NO:16, b is an integer of 15 to 545, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:16, and where b is greater than or equal to a + 14.	
558983	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 609 of SEQ ID NO:17, b is an integer of 15 to 623, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:17, and where b is greater than or equal to a + 14.	
572943	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 545 of SEQ ID NO:18, b is an integer of 15 to 559, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:18, and where b is greater than or equal to a + 14.	
585892	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1341 of SEQ ID NO:19, b is an integer of 15 to 1355, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:19, and where b is greater than or equal to a + 14.	
589390	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1266 of SEQ ID NO:20, b is an integer of 15 to 1280, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:20, and where b is greater than or equal to a + 14.	T47628, T49403, T49829, T49830, T50800, T50963, T51976, T55846, T55860, T55896, T55911, T58744, T58811, T58891, T59252, T59279, T59293, T59615, T59690, T59727, T59826, T60434, T60514, T60584, T61357, T40352, T62559, T62688, T62839, T63122, T64603, T64640.

		T67682. T67756, T68181, T68439, T68506. T68606, T68718, T68783, T68839. T68849. T68976, T69049, T71223. T71347. T71509, T71853, T71858, T71938. T72197, T72264, T72414, T72471, T72923, T73204, T73259, T73283, T73446, T73607, T73621, T73645, T73713, T73744, T73772, T73796, T74114, T74545, T74599, T87829, T90307, T90394, T91481, T92437, T92617, T81767, T82080, R27059, R27060, R31693, R31735. R50548, R50646, R64321, R64322, R75660. R75768, R75866, R76038, R79765, R79766, H22209, H24391, H25902, H27236, H28585, H29860, H29954, H41994, H42226, H42298, H43069, H43893, H43934, R83465, R84983, R94905, R94988, R96360, R96403, R97059,.R98674, R98900, R99186, R99187, H50701, H50801. H57754, H62182, H63649, H63650, H64755, H64756, H69075, H70056, H70057, H70855, H70856, H71581, H75758, H75893, H80974, H80975, H83141, H83142, H83271, H85046, H84668, H91780, H92207, H92350, H94891, H94943, H94966, H95486, H99418, N52264, N58261, N74184, N77638, N81021, N92261, N99137, W04350, W07850, W16893, W39467, W45038, W47174, W47433, W52853, W63782, W67635, W67759, W67868, W67881, W93706, W94183, W96351, W96352, N89587, AA012898, AA019884, AA020863, AA025865, AA025866. AA056092, AA057434, AA070445, AA192155, AA192879, AA226741, AA227477
596882	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1177 of SEQ ID NO:21, b is an integer of 15 to 1191, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:21, and where b is greater than or equal to a + 14.	
616289	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 839 of SEQ ID NO:22, b is an integer of 15 to 853, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:22, and where b is greater than or equal to a + 14.	
622140	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide	W39497, W52751, AA099814, AA128882. AA173072, AA226739

	sequence described by the general formula of a-b, where a is any integer between 1 to 460 of SEQ ID NO:23, b is an integer of 15 to 474, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:23, and where b is greater than or equal to a + 14.	
623566	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 2266 of SEQ ID NO:24, b is an integer of 15 to 2280, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:24, and where b is greater than or equal to a + 14.	
647714	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1047 of SEQ ID NO:25, b is an integer of 15 to 1061, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:25, and where b is greater than or equal to a + 14.	
647752	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1558 of SEQ ID NO:26, b is an integer of 15 to 1572, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:26, and where b is greater than or equal to a + 14.	
651774	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1991 of SEQ ID NO:27, b is an integer of 15 to 2005, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:27, and where b is greater than or equal to a + 14.	T69901, T69949, T70775, R20554, R33030, R33917, R48406, H58331, H58720, H67041, H68124, H93586, H94430, H94513, H97468, H99219, N23459, N26334, N35428, N49203, N50256, N64246, N93349, W19550, W19996, W25330, W73940, W77984, W93791, W94028, N90424, AA025537, AA025680, AA025371, AA026317, AA026318, AA084549, AA086048, AA086130, AA098995, AA099068, AA115309, AA136486, AA151843, AA149689, AA148825, AA150406, AA150425, AA173377
651995	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1394 of SEQ ID NO:28, b is an integer of 15 to 1408, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:28, and where b is greater than or equal to a + 14.	
652156	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 903 of SEQ ID NO:29, b is an integer of 15 to 917, where both a and	T40364, R22492, R49907, R49908, R62310, R62311, R65652, R67030, R81699, R81700, H18589, H20024, H20099, H20123, H20797, H22404, H22615, H25816, H27051, H42294,

	b correspond to the positions of nucleotide residues shown in SEQ ID NO:29, and where b is greater than or equal to a + 14.	H44827, H49661, H51422, H51465, H56482, H56483, H70295, H86037, H93528, H93860, H96113, H96114, N22715, N31188, N33831, N54495, N70601, N70623, N76607, N78626, W04920, W05505, W07305, W15350, W39442, W60859, W60860, W72726, W76452, AA017463, AA024543, AA024544, AA026421, AA026498, AA027270, AA034429, AA046316, AA046142, AA053920, AA056230, AA063244, AA062885, AA085305, AA128171, AA126216, AA149890, AA150552, AA187825, AA188597, AA417004, AA417190
653010	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 563 of SEQ ID NO:30, b is an integer of 15 to 577, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:30, and where b is greater than or equal to a + 14.	
655904	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 2045 of SEQ ID NO:31, b is an integer of 15 to 2059, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:31, and where b is greater than or equal to a + 14.	T61561, T90265, T90707, R09280, R17627, R43348, R54854, R54658, H20872, H27229, H64571, H64673, H64571, N47495, N54722, N75461, W73679, AA010711, AA010712, AA082107, AA130516, AA132052, AA132156, AA147852, AA147908, AA148276, AA148277, AA181933, AA187549, AA187845, AA186675, AA188310, AA193212
657852	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 535 of SEQ ID NO:32, b is an integer of 15 to 549, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:32, and where b is greater than or equal to a + 14.	
666414	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 827 of SEQ ID NO:33, b is an integer of 15 to 841, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:33, and where b is greater than or equal to a + 14.	
667847	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 849 of SEQ ID NO:34, b is an integer of 15 to 863, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:34, and where b is greater than or equal to a + 14.	T47009, T47010, T55133, T55301, T57663, T57702, T59664, T59797, T59800, T49370, T72020, T26631, R22343, R46325, R48879, R50151, R50204, R55208, R71485, R71535, R72144, R72362, R72553, R74062, H13587, H16167, H18121, H20172, H20361, H22514, H40774, H40775,

		H42435, H42865, H43100, H43164, H45140, H45441, H46013, H46083, H46159, R97084, R97131, H56498, H60260, H60567, H67238, H71802, H77325, H77338, H81556, H87775, H87825, H91889, H92057, H93187, H96056, H96420, H81556, H99575, N21484, N23829, N24221, N26831, N27079, N27278, N27582, N30213, N30255, N31642, N31989, N31996, N32655, N32790, N35515, N38983, N39859, N40012: N40488, N41792, N41978, N54988, N57097, N70071, N77176, N78930, N80037, N80573, N81058, N92768, N93810, W07000, W07659, W07868, W44961, W44962, W58175, W58263, W58182, AA001206, AA017579, AA026640, AA026706, AA057605, AA058758, AA082491, AA084088, AA086460, AA100968, AA112029, AA121337, AA121500, AA130704, AA130790, AA152420, AA156094, AA156123, AA181929, AA182575, AA182617, AA186931, AA195982, AA253952, AA283976, AA426098, AA425122, AA428823, AA429359
670188	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1216 of SEQ ID NO:35, b is an integer of 15 to 1230, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:35, and where b is greater than or equal to a + 14.	
670279	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 626 of SEQ ID NO:36, b is an integer of 15 to 640, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:36, and where b is greater than or equal to a + 14.	T50781, T51265, T55324, T56327
670729	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 583 of SEQ ID NO:37, b is an integer of 15 to 597, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:37, and where b is greater than or equal to a + 14.	
674123	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 610 of SEQ ID NO:38, b is an integer of 15 to 624, where both a and b correspond to the positions of nucleotide residues	

	shown in SEQ ID NO:38, and where b is greater than or equal to a + 14.	
676496	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1015 of SEQ ID NO:39, b is an integer of 15 to 1029, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:39, and where b is greater than or equal to a + 14.	
678162	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1093 of SEQ ID NO:40, b is an integer of 15 to 1107, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:40, and where b is greater than or equal to a + 14.	T40233, T40521, T41098, T47133, T47529, T49156, T49157, T51636, T55352, T55402, T55422, T57649, T59314, T62530, T62806, T62954, T72271, T73592, T89655, T78884, R19194, R89249, R93164, H57861, H93645, N22493, N26661, N32984, N63146, N66448, N67443, N69984, N72141, N77952, N78933, N81091, N95826, W02074, W24850, W24972, W38365, W44897, W57997, W58080, W65414, W65435, W74634, AA007562, AA009767, AA022918, AA022939, AA025169, AA029717, AA029656, AA032096, AA040581, AA046091, AA070493, AA070646, AA070707, AA071405, AA071414, AA074752, AA075706, AA075696, AA079282, AA085620, AA100126, AA126795, AA128838, AA136579, AA143069, AA143200, AA146637, AA147370, AA147705, AA156001, AA157342, AA161090, AA164798, AA179749, AA187235, AA188048, AA187029, AA188384, AA192271, AA196973, AA235468, AA243180, AA459416, AA459642
678248	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1037 of SEQ ID NO:41, b is an integer of 15 to 1051, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:41, and where b is greater than or equal to a + 14.	
683668	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 2178 of SEQ ID NO:42, b is an integer of 15 to 2192, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:42, and where b is greater than or equal to a + 14.	T49549, T49550, T49700, T49912, T49937, T50912, T51558, T53285, T53375, T53376, T53721, T54314, T54840, T55217, T56413, T99069, T99669, R01522, R31653, R32820, R32921, R35743, R50997, R64077, R65723, R69349, R71009, R72798, R72824, R76854, R77142, R79240, R79511, R80194, R80295, R81155, H39823, H39824, R84909, R85592, R91193, H50793, H52341, H53594, H53916, H92997, N26572, N32090,

		N32406, N34179, N36271, N45401, N49216, N50267, N67233, N67568, N72254, N75478, N93355, N94504, W00543, W05288, W05816, W23954, W24625, W24650, W25354, W49666, W52302, AA121852, AA121851, AA128593, AA128712, AA136731, AA136688, AA167235, AA167584, AA173693, AA176648, AA176804, AA179999, AA181456, AA181457, AA256158, AA256215, AA256247, AA458729, AA458778, AA464936, AA464937
693172	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 339 of SEQ ID NO:43, b is an integer of 15 to 353, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:43, and where b is greater than or equal to a + 14.	T49005, T50129, T54766, T59468, T71241, T89633, R66699, R67578, H25853, H26090, H41256, H43182, H45273, N58288, N95319, AA054338, AA057604, AA084261
694303	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 3476 of SEQ ID NO:44, b is an integer of 15 to 3490, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:44, and where b is greater than or equal to a + 14.	
695042	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 767 of SEQ ID NO:45, b is an integer of 15 to 781, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:45, and where b is greater than or equal to a + 14.	
699799	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1417 of SEQ ID NO:46, b is an integer of 15 to 1431, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:46, and where b is greater than or equal to a + 14.	T50599, R25615, R31078, R68513, R70896, R75848, R76864, R76865, H01087, H26949, H63077, H75713, H75642, H95014, H98885, N24938, N33815, N47174, N47897, N51152, N53997, N59590, N62387, N63017, N67836, N69948, N78655, N79355, N94343, N98329, W01767, W03440, W15144, W19292, W25534, W37911, W42857, W42912, W48630, W72791, W76438, W81113, W80546, W80525, W80526, W84575, W84645, AA010674, AA011261, AA026981, AA031662, AA039737, AA039810, AA040524, AA040523, AA046308, AA046396, AA099365, AA101915, AA129310, AA129354, AA131951, AA186409
702216	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide	T64167, T64355, T68409, T68475, T73691, T73717, T97735, T97840,

	sequence described by the general formula of a-b, where a is any integer between 1 to 1899 of SEQ ID NO:47, b is an integer of 15 to 1913, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:47, and where b is greater than or equal to a + 14.	T98899, T99491, R00460, R01214, R01326, H45786, R93124, R96609, H61118, H61119, H61454, H62460, H64003, H64052, H91078, H91378, N58480, N64695, N65991, N74260, N78070, N79244, N91708, N95101, W03761, W04301, N90479, AA130077, AA130076, AA152275, AA150441
703015	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1747 of SEQ ID NO:48, b is an integer of 15 to 1761, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:48, and where b is greater than or equal to a + 14.	R72819, R73270, H43839, W47195, W52204, AA242894, AA424584, AA424629
706391	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 942 of SEQ ID NO:49, b is an integer of 15 to 956, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:49, and where b is greater than or equal to a + 14.	T48974, H26922, H30342, H44743, H45233, R88178, H81778, H92363, N29006, N44860, N46515, AA079547, AA158434, AA160590, AA428285
706892	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 549 of SEQ ID NO:50, b is an integer of 15 to 563, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:50, and where b is greater than or equal to a + 14.	
706924	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 3201 of SEQ ID NO:51, b is an integer of 15 to 3215, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:51, and where b is greater than or equal to a + 14.	T68892, T68966, T75421, R15205, R16398, R41650, R42339, R52995, R52996, R41650, H12000, H16753, H16861, H27652, H27653, H27982, H28497, H29323, H29416, H85752, H98511, N22580, N24339, N28586, N42727, N50084, N75803, N78815, W07245, W21306, W23840, W57924, W58128, W72277, W76304, W86460, AA002243, AA002080, AA025565, AA025683, AA026606, AA026718, AA150696, AA150801
707642	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 612 of SEQ ID NO:52, b is an integer of 15 to 626, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:52, and where b is greater than or equal to a + 14.	
710369	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 906 of SEQ ID NO:53, b is an integer of 15 to 920, where both a and	T48815, T60685, T91108, T99835, AA150217, AA157340, AA157240, AA171947

	b correspond to the positions of nucleotide residues shown in SEQ ID NO:53, and where b is greater than or equal to a + 14.	
718826	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1076 of SEQ ID NO:54, b is an integer of 15 to 1090, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:54, and where b is greater than or equal to a + 14.	
719790	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1450 of SEQ ID NO:55, b is an integer of 15 to 1464, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:55, and where b is greater than or equal to a + 14.	T47380, T47538, T47539, T53445, T53446, T54910, T55077, T59959, T60032, T62504, T62649, T63049, T63297, T63382, T65688, T71591, T71742, T93094, T93187, T94131, T94222, T91210, T84959, T99044, T99045, R26119, R26148, R33224, R35866, R36526, R53923, R53924, R69596, R69684, R76209, R76210, R79249, R79521, H03427, H03507, H12529, H13501, H19016, H19310, H21587, H21652, H21653, H30119, H39693, H42698, H46635, R93371, R98210, R99855, H54120, H54786, H54837, H58991, H65355, H65566, H67613, H72632, H74102, H95312, N48235, N58029, N64226, N66907, N70763, N78303, N93848, N94316, N95432, N98433, W01816, W02218, W05772, W21419, W24044, W24297, W30823, W32382, W37228, W37317, W40321, W42528, W46445, W49731, W51944, W53011, W53012, W60051, W60129, W60154, W68332, W68216, W72730, W74593, W92813, W93310, AA010985, AA011307, AA031435, AA035708, AA037040, AA053073, AA053374, AA055567, AA069724, AA069690, AA069682, AA069900, AA069951, AA070693, AA071421, AA074606, AA075555, AA075673, AA075544, AA081017, AA081251, AA081428, AA082119, AA082022, AA082213, AA082241, AA082247, AA082400, AA082365, AA082438, AA082679, AA083225, AA083266, AA083508, AA083411, AA083637, AA084202, AA099623, AA102015, AA099659, AA100102, AA100163, AA100429, AA100430, AA100455, AA100456, AA100711, AA100764, AA100906, AA100919, AA100963, AA101118, AA102494, AA101184, AA112123, AA122359, AA122360, AA126882, AA127103, AA128195, AA128674, AA128686, AA128741,

		AA128747, AA128785, AA133488, AA133489, AA130006, AA130007, AA134211, AA130492, AA130507, AA134345, AA134346, AA134457, AA134458, AA134461, AA134462, AA130907, AA131020, AA131973, AA132141, AA132493, AA132601, AA134904, AA135121, AA135182, AA135348, AA136318, AA143066, AA143256, AA143278, AA143386, AA146650, AA146835, AA146836, AA146860, AA146861, AA146870, AA146871, AA146918, AA147716, AA147707, AA147868, AA148130, AA148090, AA148091, AA152422, AA148435, AA148867, AA148492, AA148702, AA151453, AA151452, AA151828, AA155801, AA155886, AA156025, AA156044, AA156053, AA156155, AA156222, AA157080, AA157168, AA157325, AA157423, AA157434, AA157471, AA157605, AA157631, AA157546, AA157775, AA157826, AA158157, AA158273, AA158888, AA158887, AA159153, AA159250, AA160104, AA159856, AA161278, AA161301, AA160817, AA164741, AA165616, AA165606, AA173037, AA173038, AA176229, AA176317, AA179185, AA179190, AA179200, AA181043, AA181262, AA181342, AA181834, AA181989, AA182794, AA187247, AA187342, AA187379, AA187470, AA187528, AA187740, AA187911, AA188028, AA186378, AA186424, AA186441, AA186442, AA186568, AA186653, AA186661, AA186703, AA186910, AA187081, AA187087, AA187078, AA187135, AA188313, AA188330, AA188342, AA190473, AA193219
720222	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 971 of SEQ ID NO:56, b is an integer of 15 to 985, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:56, and where b is greater than or equal to a + 14.	AA056718, AA428747
724033	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1232 of SEQ ID NO:57, b is an integer of 15 to 1246, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:57, and where b is greater than or equal to a + 14.	N50855, AA076233, AA076232

724767	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1952 of SEQ ID NO:58, b is an integer of 15 to 1966, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:58, and where b is greater than or equal to a + 14.	
727065	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1597 of SEQ ID NO:59, b is an integer of 15 to 1611, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:59, and where b is greater than or equal to a + 14.	T26554, R31862, R31869, R67140, R70861, H00137, H23051, H23350, H60670, N28391, N28646, AA081571
727246	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1835 of SEQ ID NO:60, b is an integer of 15 to 1849, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:60, and where b is greater than or equal to a + 14.	
727932	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 219 of SEQ ID NO:61, b is an integer of 15 to 233, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:61, and where b is greater than or equal to a + 14.	
731167	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 2319 of SEQ ID NO:62, b is an integer of 15 to 2333, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:62, and where b is greater than or equal to a + 14.	
732514	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1456 of SEQ ID NO:63, b is an integer of 15 to 1470, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:63, and where b is greater than or equal to a + 14.	
734080	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 925 of SEQ ID NO:64, b is an integer of 15 to 939, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:64, and where b is greater than or equal to a + 14.	
734288	Preferably excluded from the present invention are	

	one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 2054 of SEQ ID NO:65, b is an integer of 15 to 2068, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:65, and where b is greater than or equal to a + 14.	
739448	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1377 of SEQ ID NO:66, b is an integer of 15 to 1391, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:66, and where b is greater than or equal to a + 14.	T53676, T53677, T54741, T55855, T55906, T56935, T57622, T58975, T58979, T61059, T61143, T90498, T90594, T93775, R07734, R07735, R40067, R75954, R75978, R76790, R76809, R77290, R77315, R77348, R79433, R79434, R97814, H50168, H70091, H77406, H80889. H82088, H82195, N33576, N39028, N48219, N49421, N52598, N66328, N67208, N73788, N78932, N92856, N99411, W07071, W17213, W24422, W25582, W47407, W47574, W49651, W49725, W68140, W68467, AA025829, AA025972, AA074731, AA074835, AA075316, AA081368, AA081369, AA082652, AA082810, AA101054, AA102495, AA115718, AA115719, AA127079, AA127080, AA127200, AA127199, AA128645, AA128813, AA133732, AA130465, AA130466, AA132111, AA143233, AA143289, AA146780, AA147706, AA148134, AA151491, AA157062, AA157046, AA157630, AA165124, AA165123, AA164625, AA165420, AA165583, AA173407, AA173462, AA179910, AA179911, AA180198, AA181087, AA181556, AA182450, AA182951, AA186670, AA188289, AA192925, AA193075, AA464823
739668	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 645 of SEQ ID NO:67, b is an integer of 15 to 659, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:67, and where b is greater than or equal to a + 14.	
740060	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 2967 of SEQ ID NO:68, b is an integer of 15 to 2981, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:68, and where b is greater than or equal to a + 14.	
741560	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b,	

	where a is any integer between 1 to 589 of SEQ ID NO:69, b is an integer of 15 to 603, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:69, and where b is greater than or equal to a + 14.	
742543	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1087 of SEQ ID NO:70, b is an integer of 15 to 1101, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:70, and where b is greater than or equal to a + 14.	
742831	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 700 of SEQ ID NO:71, b is an integer of 15 to 714, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:71, and where b is greater than or equal to a + 14.	
745327	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 2876 of SEQ ID NO:72, b is an integer of 15 to 2890, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:72, and where b is greater than or equal to a + 14.	
745695	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 2474 of SEQ ID NO:73, b is an integer of 15 to 2488, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:73, and where b is greater than or equal to a + 14.	T56303, T58644, T58694, R48815, R48816, R68140, R74376, R78015, R81014, H00852, H01233, H17193, H17969, H25101, H27005, H30607, H41236, H42218, H42290, H42904, H42977, H45271, H45342, R83816, R98855, R98939, H53696, H62059, H82544, H83097, N40713, N92791, W19377, AA025571, AA053695, AA053675, AA069167, AA069166, AA076604, AA076603, AA079426, AA100088, AA099771, AA130265, AA158402, AA179641, AA235643, AA253454, AA250758, AA458951, AA458978, AA459194, AA419280, AA419329, AA425117, AA430664
750316	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 697 of SEQ ID NO:74, b is an integer of 15 to 711, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:74, and where b is greater than or equal to a + 14.	
750522	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 892 of SEQ ID	

	NO:75, b is an integer of 15 to 906, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:75, and where b is greater than or equal to a + 14.	
750583	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 257 of SEQ ID NO:76, b is an integer of 15 to 271, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:76, and where b is greater than or equal to a + 14.	
751020	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 659 of SEQ ID NO:77, b is an integer of 15 to 673, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:77, and where b is greater than or equal to a + 14.	N80268, N95387, W57806, W63590, AA182782, AA187759, AA199806, AA262640, AA262111, AA262106, AA460214
752196	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 353 of SEQ ID NO:78, b is an integer of 15 to 367, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:78, and where b is greater than or equal to a + 14.	R67541
753084	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1330 of SEQ ID NO:79, b is an integer of 15 to 1344, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:79, and where b is greater than or equal to a + 14.	T93791, T93840, R77826, R78199, R99272, H54274, H65600, H67128, H75533, H75532, H81433, N57836, N58786, N72699, N77475, W02480, W78743, W80625, W90276, AA007397, AA127528, AA127529, AA130419, AA147733, AA150095, AA195008, AA195060
754957	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 3734 of SEQ ID NO:80, b is an integer of 15 to 3748, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:80, and where b is greater than or equal to a + 14.	
756557	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1877 of SEQ ID NO:81, b is an integer of 15 to 1891, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:81, and where b is greater than or equal to a + 14.	
756712	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1940 of SEQ ID NO:82, b is an integer of 15 to 1954, where both a	

	and b correspond to the positions of nucleotide residues shown in SEQ ID NO:82, and where b is greater than or equal to a + 14.	
757414	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 922 of SEQ ID NO:83, b is an integer of 15 to 936, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:83, and where b is greater than or equal to a + 14.	T49651, T49652, T92946, T93013, H02307, H02419, N42072, AA169576
757614	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1499 of SEQ ID NO:84, b is an integer of 15 to 1513, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:84, and where b is greater than or equal to a + 14.	T93709, T96172, H00439, H00480, R85176, H51264, H51834, H53645, H57470, H57991, H73334, N33138, N42318, N94987, AA028955, AA081550, AA082013, AA113225, AA113810, AA133619, AA133522, AA132699, AA132810, AA151877, AA149662, AA157324, AA157422, AA159905, AA165014, AA165442, AA165443, AA167837, AA166621, AA166924, AA195339, AA195338, AA252790
757815	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1284 of SEQ ID NO:85, b is an integer of 15 to 1298, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:85, and where b is greater than or equal to a + 14.	
759878	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1995 of SEQ ID NO:86, b is an integer of 15 to 2009, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:86, and where b is greater than or equal to a + 14.	
760227	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 520 of SEQ ID NO:87, b is an integer of 15 to 534, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:87, and where b is greater than or equal to a + 14.	
760312	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 4288 of SEQ ID NO:88, b is an integer of 15 to 4302, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:88, and where b is greater than or equal to a + 14.	
766051	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide	T57753, T60650, R11036, R11084, R00826, R01482, H87221, N25112,

	sequence described by the general formula of a-b, where a is any integer between 1 to 2768 of SEQ ID NO:89, b is an integer of 15 to 2782, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:89, and where b is greater than or equal to a + 14.	N33451, N42424, N47338, N48186, N62628, N68902, N71490, N78399, N99533, W16943, W78948, W85915, W95743, N89568, AA039230, AA039231, AA047564, AA047582, AA047702, AA047752, AA120926, AA126453, AA135549, AA135529, AA429718
767593	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1023 of SEQ ID NO:90, b is an integer of 15 to 1037, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:90, and where b is greater than or equal to a + 14.	T51635, T57709, T61468, T63793, T63818, T92894, T92984, T94396, T75475, T75508, T87575, T79848, T85949, R25644, R27489, R70702, R78772, H44836, H44835, R84349, R86157, R89703, R99494, H48567, H48836, H57859, H83579, H86373, H86690, H88284, H97937, H98241, H99117, H99249, N24363, N24573, N26374, N27129, N31662, N36546, N40064, N45098, N45108, N53503, N59526, N63219, N64179, N64178, N66660, N70536, N72298, N98943, W02894, W19364, W60295, W60386, W72691, W77806, W93582, W93631, W92326, W92382, N90765, AA001997, AA013356, AA017023, AA017221, AA018780, AA026639, AA026705, AA029569, AA029496, AA029736, AA035387, AA035694, AA044958, AA055558, AA063564, AA100726, AA100744, AA134118, AA130301, AA151965, AA233192, AA253060, AA253117
768053	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1038 of SEQ ID NO:91, b is an integer of 15 to 1052, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:91, and where b is greater than or equal to a + 14.	
768055	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1220 of SEQ ID NO:92, b is an integer of 15 to 1234, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:92, and where b is greater than or equal to a + 14.	T68053, R09316, R09788, T84929, R24826, R66259, R68879, R80029, H00967, H89841, H96162, N39802, N44634, N68319, N70487, N71145, N72732, W01594, W52285, W73342, W85800, AA022906, AA022975, AA031962, AA032044, AA032163, AA037604, AA043694, AA043695, AA044134, AA074287, AA081041, AA081042, AA082218, AA082461, AA082475, AA083977, AA100460, AA155926, AA167365, AA171958, AA173534, AA187036, AA224429
769685	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1557 of SEQ ID	

	NO:93. b is an integer of 15 to 1571, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:93, and where b is greater than or equal to a + 14.	
771920	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1858 of SEQ ID NO:94, b is an integer of 15 to 1872, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:94, and where b is greater than or equal to a + 14.	
772790	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1502 of SEQ ID NO:95, b is an integer of 15 to 1516, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:95, and where b is greater than or equal to a + 14.	
772916	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1756 of SEQ ID NO:96, b is an integer of 15 to 1770, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:96, and where b is greater than or equal to a + 14.	
773225	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 924 of SEQ ID NO:97, b is an integer of 15 to 938, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:97, and where b is greater than or equal to a + 14.	
773632	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 297 of SEQ ID NO:98, b is an integer of 15 to 311, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:98, and where b is greater than or equal to a + 14.	
774364	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 606 of SEQ ID NO:99, b is an integer of 15 to 620, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:99, and where b is greater than or equal to a + 14.	W01405, AA172322
775355	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 2497 of SEQ ID NO:100, b is an integer of 15 to 2511, where both a	T49285, T61774, T68350, T68396, T94414, T69842, T81078, R01216, R05674, R21522, R21626, R23745, R23797, R24081, R24137, R24753, R32662, R36359, R45484, R45484,

	and b correspond to the positions of nucleotide residues shown in SEQ ID NO:100, and where b is greater than or equal to a + 14.	R63380, R63433, R70942, R70995, R73973, R78964, H08973, H09543, H16712, H16713, H20846, H20896, R99241, H82276, H82382, H84715, H85367, H85516, H89615, H95047, H96450, H97881, N20953, N21537, N22201, N25769, N29477, N30442, N37087, N42334, N42354, N66424, N66864, N67873, N71242, N73740, N94555, N99903, W45394, W46993, W46961, W46960, W46881, W73247, W90778, AA026678, AA026215, AA043908, AA044414, AA042828, AA062957, AA076063, AA121145, AA121476, AA195131, AA234043, AA234044, AA426421
775844	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 2967 of SEQ ID NO:101, b is an integer of 15 to 2981, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:101, and where b is greater than or equal to a + 14.	T73286, T66741, T66742, R12147, R15080, R19321, R39271, R42973, R44589, R44589, H06197, H08725, R94752, H71652, H71653, H79764, H79765, H79770, H79762, H79761, H79771, H92246, H96184, N45199, W93244, W93245, W93258, W93257, W94615, W94654, AA001180, AA039582, AA039689, AA082198, AA157370, AA157869, AA253368
777760	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 2790 of SEQ ID NO:102, b is an integer of 15 to 2804, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:102, and where b is greater than or equal to a + 14.	
779837	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 708 of SEQ ID NO:103, b is an integer of 15 to 722, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:103, and where b is greater than or equal to a + 14.	T67628, T72838, H59238, H84693, N80048, W07009, W37555, W39191, N90251, AA057629
780769	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1622 of SEQ ID NO:104, b is an integer of 15 to 1636, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:104, and where b is greater than or equal to a + 14.	T66609, T66610, T83560, R15983, R15984, R35702, R49338, R49338, H11613, R94244, H87098, H87745, W60710, W60772, W94034, AA258151, AA258913, AA425943
781445	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1547 of SEQ ID NO:105, b is an integer of 15 to 1561, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:105, and where b is	

	greater than or equal to a + 14.	
781531	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 472 of SEQ ID NO:106, b is an integer of 15 to 486, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:106, and where b is greater than or equal to a + 14.	
783018	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 786 of SEQ ID NO:107, b is an integer of 15 to 800, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:107, and where b is greater than or equal to a + 14.	R18976
783097	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1044 of SEQ ID NO:108, b is an integer of 15 to 1058, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:108, and where b is greater than or equal to a + 14.	
784198	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1062 of SEQ ID NO:109, b is an integer of 15 to 1076, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:109, and where b is greater than or equal to a + 14.	
784868	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1185 of SEQ ID NO:110, b is an integer of 15 to 1199, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:110, and where b is greater than or equal to a + 14.	
785428	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 3616 of SEQ ID NO:111, b is an integer of 15 to 3630, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:111, and where b is greater than or equal to a + 14.	T47751, T39348, T39359, T98137, T79193, T95760, R16653, R16654, R24052, R24245, R33230, R44846, R50794, R50912, R44846, R60930, R61049, R71116, R71620, R77888, R80860, H00109, H04333, H04688, H05041, H09555, H30257, H30320, H47931, R94218, R99062, R99260, H50702, H50803, H52629, H52628, H54000, H67115, H70269, H83460, H83572, H84911, H99358, N21482, N21632, N24626, N33762, N41609, N67949, N69593, N70188, N71452, N71818, N77888, N79031, N99501, W02150, W03072, W05781, W19647, W19972, W20125, W30896, W33043,

		W33197, W35407, W37262, W39072, W47654, W52846, W56143, W60064, W60074, W65501, W67522, W67591, W69745, W69926, W80811, W94093, W94156, N90996, AA039462, AA040857, AA043084, AA043810, AA053423, AA053042, AA064625, AA064709, AA115540, AA115051, AA120833, AA129500, AA129499, AA146736, AA148602, AA152314, AA150343, AA150620, AA150790, AA157282, AA160296, AA173937, AA173969, AA181340, AA188207, AA186354, AA188646, AA190484, AA199676, AA199677, AA243342, AA250981, AA459647, AA459773, AA460227
785845	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1512 of SEQ ID NO:112, b is an integer of 15 to 1526, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:112, and where b is greater than or equal to a + 14.	
785854	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 571 of SEQ ID NO:113, b is an integer of 15 to 585, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:113, and where b is greater than or equal to a + 14.	T85881, W45204
786705	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 487 of SEQ ID NO:114, b is an integer of 15 to 501, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:114, and where b is greater than or equal to a + 14.	R09422
787186	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1951 of SEQ ID NO:115, b is an integer of 15 to 1965, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:115, and where b is greater than or equal to a + 14.	
787279	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1046 of SEQ ID NO:116, b is an integer of 15 to 1060, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:116, and where b is greater than or equal to a + 14.	T62081, T97170, R17585, R42923, R48789, R48896, R54561, R54562, R54721, R54722, R42923, R72984, R73595, H23901, H43508, H46275, H46348, H47255, H47254, R83475, R89352, R91048, R93150, R93669, R94520, R98839, H48417, H48899, H48900, H50560, H54157, H58936,

		H58983, H67630, H69455, H72554, H72955, H89822, N23388, N33070, N35168, N40256, N44641, N52556, N59706, N68387, N80806, N92514, W17007, W19578, W20217, W38835, W49822, W56061, W65416, W65285, N90575, AA002190, AA045344, AA045446, AA052950, AA053432, AA082245, AA083753, AA102071, AA099961, AA101574, AA112070, AA125782, AA125931, AA135139, AA135268, AA146635, AA151603, AA149484, AA149981, AA152120, AA171975, AA172123, AA181805, AA181821, AA188148, AA188225, AA186556, AA186917, AA460297, AA461585
789002	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 695 of SEQ ID NO:117, b is an integer of 15 to 709, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:117, and where b is greater than or equal to a + 14.	
789008	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 2039 of SEQ ID NO:118, b is an integer of 15 to 2053, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:118, and where b is greater than or equal to a + 14.	T47492, T47493, T47900, T48303, T48445, T48456, T49007, T49079, T49080, T49218, T49310, T49311, T49913, T49914, T49941, T51256, T51337, T51371, T51423, T51604, T51757, T52271, T52400, T53326, T53327, T54148, T54244, T54295, T54330, T54402, T54407, T55485, T55733, T56237, T56379, T56414, T56565, T39384, T40546, T40551, T40552, T40824, T89603, T79470, T79561, R01378, R12635, R20536, R21209, R21238, R21239, R22062, R22119, R22190, R22241, R22534, R22535, R22823, R23625, R23881, R24090, R25741, R26431, R26587, R28327, R28328, R28330, R31619, R32132, R32349, R33134, R33286, R35454, R36658, R39739, R50498, R50581, R20536, R56656, R65717, R65777, R65870, R67856, R67857, R68076, R69399, R69531, R69752, R69920, R71289, R72350, R74061, R77148, R77149, R80495, R80640, R82550, H00862, H01301, H01472, H01571, H02637, H02893, H03072, H03073, H03443, H03525, H03812, H03836, H23457, H23458, H26513, H26583, H26584, R86226, R86227, R87053, R91130, R91174, R92513, R92642, R93418, R93468, R93700, R94462, R94463, R94793, R95110,

		R96330, R96329, R96675, R96943, R97000, R98195, R99857, H48277, H48366, H48451, H53119, H54247, H54246, H57144, H57217, H58791, H59276, H59324, H59614, H59654, H62873, H62997, H66302, H67109, H67468, H67594, H67634, H67646, H67685, H67891, H67935, H68007, H68476, H72996, H73208, H73882, H74057, H74076, H74196, H75522, H75366, H77704, H77705, H78593, H79262, H79373, H81287, H81343, H82036, H82218, H82313, H87010, H87011, H90552, H90551, H93198, H94403, N28269, N30773, N34862, N38975, N38989, N39317, N43935, N45164, N48122, N48136, N50666, N50756, N52570, N53559, N53589, N55006, N55026, N57654, N58258, N58340, N58627, N58738, N70218, N72552, N72649, N77216, N77511, N77635, N80637, W01074, W58701, W68231, W68232, W68700, W72561, W72580, W72399, W76223, W85725, W92304, W92318, W92144, W92354, AA004478, AA004551, AA009715, AA009825, AA024464, AA024465, AA025660, AA039523, AA039522, AA040081, AA040128, AA040033, AA040827, AA045744, AA053323, AA099152, AA099250
789555	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1810 of SEQ ID NO:119, b is an integer of 15 to 1824, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:119, and where b is greater than or equal to a + 14.	T85669, H62189, H62190, H73963, H73295, N74147, W04314, W23625, W35215, AA040573, AA040671
789631	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 592 of SEQ ID NO:120, b is an integer of 15 to 606, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:120, and where b is greater than or equal to a + 14.	
789779	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 824 of SEQ ID NO:121, b is an integer of 15 to 838, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:121, and where b is greater than or equal to a + 14.	N69694, AA151932
790387	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide	H19654, H87102, H87749, N29354, N34298, N44187, N57052, W69612,

	sequence described by the general formula of a-b. where a is any integer between 1 to 642 of SEQ ID NO:122, b is an integer of 15 to 656. where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:122, and where b is greater than or equal to a + 14.	W93844, W93865, AA027893. AA029638, AA058317. AA058495, AA179870. AA232827, AA233881, AA235809
790461	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1372 of SEQ ID NO:123, b is an integer of 15 to 1386, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:123, and where b is greater than or equal to a + 14.	R66275, R76171, R82537, AA054476, AA056199, AA127010, AA143025, AA151006, AA150976
790931	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 831 of SEQ ID NO:124, b is an integer of 15 to 845, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:124, and where b is greater than or equal to a + 14.	T92052, R10686, T84927, R21818, R22331, R22332, R22401, R23139, R23140, R23369, R32153, R32154, R63527, R63575, R68799, R68901, R80768, H12779, H12836, H56522, H56704, H94832, H96055, H96058, H96422, H96418, N26715, N27088, N31910, N32532, N33383, N34596, N42693, N42748, W32121, W37432, W44577, W44627, W51792, W61294, W65390, AA026773, AA026774
791176	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1642 of SEQ ID NO:125, b is an integer of 15 to 1656, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:125, and where b is greater than or equal to a + 14.	T51708, T51919, T69384, R50942, R73632, R73706, H28125, N22822, N78772
791983	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 823 of SEQ ID NO:126, b is an integer of 15 to 837, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:126, and where b is greater than or equal to a + 14.	
792539	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1203 of SEQ ID NO:127, b is an integer of 15 to 1217, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:127, and where b is greater than or equal to a + 14.	H53623, H53662, N23079, N69293, N89689, AA034518, AA035409, AA035410, AA046490, AA046762, AA085037, AA085105, AA134976, AA135078, AA459951, AA460040
792749	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1335 of SEQ ID NO:128, b is an integer of 15 to 1349, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:128, and where b is greater than or equal to a + 14.	R13058, R13951, R40011, R51765, R51766, R40011, R67629, R67630, H01808, H29310, H29403, R99196, H52742, H52788, H61636, H71767, H71768, N20919, N27779, N36030, N41741, N47900, N55480, N76967, W21551, W44410, W44331, W46458, W46528, W46810, W46928, W51766,

		W57869, W58140, W86456, N90422, AA029174, AA029253, AA031374, AA031375, AA062913, AA082549, AA133965, AA167773, AA166872, AA176295, AA176395, AA428235
792961	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 2304 of SEQ ID NO:129, b is an integer of 15 to 2318, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:129, and where b is greater than or equal to a + 14.	
793206	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 2135 of SEQ ID NO:130, b is an integer of 15 to 2149, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:130, and where b is greater than or equal to a + 14.	
793249	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1006 of SEQ ID NO:131, b is an integer of 15 to 1020, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:131, and where b is greater than or equal to a + 14.	T48358, T48359, T71001, T71063, T72193, T72972, T67531, T69528, T86709, T86804, T89854, T90890, T91159, T85694, T85895, T95466, T95467, R00007, R00008, R12353, R23932, R23933, R37279, R63973, R64080, R73825, R73826, R76905, R77073, R77445, R77538, R79797, R79808, R79894, R79908, H11925, H11926, H15192, H16754, H16862, H19737, H20072, H21725, H22675, H24523, H26125, H26391, H39766, H41271, H41373, H41374, H43544, H43545, H44881, H45180, H45181, R92671, R94833, H57801, H58122, H58123, H62248, H62337, H69587, H69586, H80840, H80930, H85462, H85747, H86829, H86902, H96591, H96708, H97829, H99614, N25266, N26147, N27161, N29792, N33452, N33767, N33906, N36535, N38816, N39177, N40101, N42935, N42425, N44530, N45252, N45445, N57801, N59012, N78685, N79046, N91819, N98480, W02726, W04566, W15191, W15596, W17335, W24253, W25723, W30937, W31253, W31429, W31674, W39685, W44989, W46619, W46654, W57768, W57804, W57841, W57622, W67135, W67136, W73878, W73364, W73441, W77815, W80810, W80903, W92682, W92512, W92513, W96375, W96526, AA001447, AA001482, AA021374, AA021375, AA037268, AA037489, AA037569, AA039708, AA040262, AA040417, AA057011,

		AA074646, AA074679, AA075303, AA088467, AA098947, AA100987, AA126026, AA126122, AA126778, AA128010, AA128034, AA136619, AA136750, AA143234, AA143291, AA143564, AA143565, AA146915, AA151446, AA151447, AA156218, AA157383, AA159151, AA173294, AA179768, AA180442, AA181155, AA181156, AA181722, AA186611, AA188254, AA190686, AA191758, AA191547, AA195441, AA223540, AA223587
793626	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 2305 of SEQ ID NO:132, b is an integer of 15 to 2319, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:132, and where b is greater than or equal to a + 14.	
794417	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1359 of SEQ ID NO:133, b is an integer of 15 to 1373, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:133, and where b is greater than or equal to a + 14.	
795197	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1643 of SEQ ID NO:134, b is an integer of 15 to 1657, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:134, and where b is greater than or equal to a + 14.	
795251	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 2346 of SEQ ID NO:135, b is an integer of 15 to 2360, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:135, and where b is greater than or equal to a + 14.	T89826, T74514, T89080, R24028, H03686, H97493, N54611, W94797, W94798, AA129537, AA190765, AA191357, AA256363, AA425151, AA429405
795752	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1028 of SEQ ID NO:136, b is an integer of 15 to 1042, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:136, and where b is greater than or equal to a + 14.	
796261	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1023 of SEQ ID	

	NO:137, b is an integer of 15 to 1037, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:137, and where b is greater than or equal to a + 14.	
796933	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1476 of SEQ ID NO:138, b is an integer of 15 to 1490, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:138, and where b is greater than or equal to a + 14.	
799424	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1670 of SEQ ID NO:139, b is an integer of 15 to 1684, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:139, and where b is greater than or equal to a + 14.	
799698	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 413 of SEQ ID NO:140, b is an integer of 15 to 427, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:140, and where b is greater than or equal to a + 14.	
800351	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 875 of SEQ ID NO:141, b is an integer of 15 to 889, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:141, and where b is greater than or equal to a + 14.	
800573	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1491 of SEQ ID NO:142, b is an integer of 15 to 1505, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:142, and where b is greater than or equal to a + 14.	
805815	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1221 of SEQ ID NO:143, b is an integer of 15 to 1235, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:143, and where b is greater than or equal to a + 14.	
806445	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1406 of SEQ ID NO:144, b is an integer of 15 to 1420, where both a	

	and b correspond to the positions of nucleotide residues shown in SEQ ID NO:144, and where b is greater than or equal to a + 14.	
810309	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1905 of SEQ ID NO:145, b is an integer of 15 to 1919, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:145, and where b is greater than or equal to a + 14.	
811022	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1365 of SEQ ID NO:146, b is an integer of 15 to 1379, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:146, and where b is greater than or equal to a + 14.	
811023	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 500 of SEQ ID NO:147, b is an integer of 15 to 514, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:147, and where b is greater than or equal to a + 14.	
811143	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 2044 of SEQ ID NO:148, b is an integer of 15 to 2058, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:148, and where b is greater than or equal to a + 14.	
811381	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1767 of SEQ ID NO:149, b is an integer of 15 to 1781, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:149, and where b is greater than or equal to a + 14.	
811595	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1695 of SEQ ID NO:150, b is an integer of 15 to 1709, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:150, and where b is greater than or equal to a + 14.	T51013, T51104, T54094, T54185, T68577, T68655, T90261, T90702, T92691, R34639, R49168, R51392, R49168, R84952, R84994, H84723, H84890, N29820, N42512, N64677, N67206, N73458, N80110, N92710, W02861, W20327, W23680, W76675, AA031294, AA062736, AA062781, AA070243, AA070244, AA084464, AA100714, AA100767, AA136726, AA136684, AA191613, AA223541, AA223589, AA252636
813000	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide	

	sequence described by the general formula of a-b, where a is any integer between 1 to 908 of SEQ ID NO:151, b is an integer of 15 to 922, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:151, and where b is greater than or equal to a + 14.	
813288	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 621 of SEQ ID NO:152, b is an integer of 15 to 635, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:152, and where b is greater than or equal to a + 14.	
813431	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 2314 of SEQ ID NO:153, b is an integer of 15 to 2328, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:153, and where b is greater than or equal to a + 14.	T94237, T89464, T89552, R09285, T78198, R14453, R15241, R15311, R21130, R33140, R33292, R40972, R46726, R42211, R40972, R46726, R66207, R67085, R73679, R73770, H12485, H19135, H22930, H24111, H26774, H26884, R89854, R89894, R92012, R92057, H53798, H61991, H61992, H64854, H65452, H73213, H74063, H79753, H79754, H80620, H80654, H81209, H81210, H84019, H84020, N35581, N68664, N73792, N91681, N92730, N99417, W20349, W46901, W52684, W60422, W61136, W61108, W61174, W68119, W73989, W79021, W79231, W80414, W80777, W80930, AA040315, AA045023, AA045024, AA045188, AA045352, AA181735, AA181799, AA223229, AA223428, AA464186, AA464780, AA428152, AA430305
813450	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1254 of SEQ ID NO:154, b is an integer of 15 to 1268, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:154, and where b is greater than or equal to a + 14.	T90954, T84401, T85262, R22109, R48652, R72000, R73453, H14261, H27403, H42017, H42018, H38149, H38150, H69302, H69397, N98775, AA148803, AA150212
813478	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 4285 of SEQ ID NO:155, b is an integer of 15 to 4299, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:155, and where b is greater than or equal to a + 14.	
813505	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 992 of SEQ ID NO:156, b is an integer of 15 to 1006, where both a and b correspond to the positions of nucleotide	

	residues shown in SEQ ID NO:156, and where b is greater than or equal to a + 14.	
815552	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1672 of SEQ ID NO:157, b is an integer of 15 to 1686, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:157, and where b is greater than or equal to a + 14.	
815606	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 4133 of SEQ ID NO:158, b is an integer of 15 to 4147, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:158, and where b is greater than or equal to a + 14.	T69152, T69213, T80080, T80327, R19043, R27520, R38534, R38898, R44031, R44031, R67769, H11493, H11852, H13644, H22161, H28042, H39529, H42500, H43488, N32678, N50022, N51861, N54126, N54677, W16972, W32896, W35293, W38598, N89624, N90277, AA027830, AA027892, AA035739, AA055806, AA069223, AA078890, AA078891, AA099437, AA099478, AA101431, AA112543, AA121794, AA129629, AA136251, AA143110, AA150576, AA157125, AA158242, AA158709, AA159976, AA160357, AA159491, AA160534, AA160629, AA165150, AA165151, AA164643, AA166799, AA169647, AA169822, AA173082, AA187009, AA224150, AA224303, AA224514, AA224513, AA224488, AA226779, AA227396, AA227518, AA232104, AA232580, AA256938, AA255494, AA429442
816048	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1228 of SEQ ID NO:159, b is an integer of 15 to 1242, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:159, and where b is greater than or equal to a + 14.	T54940, T59322, R35627, R46514, R48419, R48536, R48537, R48569, R48582, R48668, R48683, R49781, R49827, R53111, R53210, R66870, R67958, R69435, R69517, R70414, R71907, R71948, R72113, R72818, R73269, R75924, R75959, R79565, R79566, R80393, H25645, H26211, H29817, H29904, H39626, H39738, H39881, H40715, H42210, H42281, H42354, H42710, H43124, R83615, R86066, R92103, R92104, R96726, R96727, H54075, H54232, H54233, H62253, H62342, H80441, H80442, H91114, H97541, H99927, N27357, N27665, N93636, W19226, W19703, W25418, W25514, W44404, W63554, W78078, N89960, AA027093, AA027132, AA045021, AA045022, AA045721, AA045720, AA046247, AA046280, AA058624, AA074786, AA074787, AA082394, AA085101, AA085282, AA100996, AA127562, AA127729, AA127784, AA128372,

		AA134954, AA143611, AA148145, AA150570, AA161257, AA182028, AA188387, AA232423, AA464270, AA464381, AA421219, AA425804, AA428372
822978	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 2215 of SEQ ID NO:160, b is an integer of 15 to 2229, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:160, and where b is greater than or equal to a + 14.	R28400, R82355, R82411, H01338, H01388, N24952, N33829, AA043471, AA043472, AA125807, AA128280, AA129405, AA133871, AA129367, AA133179, AA133312, AA131385, AA428408
823616	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1906 of SEQ ID NO:161, b is an integer of 15 to 1920, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:161, and where b is greater than or equal to a + 14.	
823981	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 2605 of SEQ ID NO:162, b is an integer of 15 to 2619, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:162, and where b is greater than or equal to a + 14.	
824364	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1405 of SEQ ID NO:163, b is an integer of 15 to 1419, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:163, and where b is greater than or equal to a + 14.	R21933, H39733, N69879, AA027031, AA100964, AA157234, AA173338
824423	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 3796 of SEQ ID NO:164, b is an integer of 15 to 3810, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:164, and where b is greater than or equal to a + 14.	
825279	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 803 of SEQ ID NO:165, b is an integer of 15 to 817, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:165, and where b is greater than or equal to a + 14.	R06729, R61520, R86829, H51131, N57993, W93696, AA423827
825442	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1564 of SEQ ID	

	NO:166, b is an integer of 15 to 1578, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:166, and where b is greater than or equal to a + 14.	
825548	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1680 of SEQ ID NO:167, b is an integer of 15 to 1694, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:167, and where b is greater than or equal to a + 14.	
825725	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1622 of SEQ ID NO:168, b is an integer of 15 to 1636, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:168, and where b is greater than or equal to a + 14.	
826639	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 653 of SEQ ID NO:169, b is an integer of 15 to 667, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:169, and where b is greater than or equal to a + 14.	
827079	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 3584 of SEQ ID NO:170, b is an integer of 15 to 3598, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:170, and where b is greater than or equal to a + 14.	
827153	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 926 of SEQ ID NO:171, b is an integer of 15 to 940, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:171, and where b is greater than or equal to a + 14.	
827351	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1444 of SEQ ID NO:172, b is an integer of 15 to 1458, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:172, and where b is greater than or equal to a + 14.	R14710, H92769, H92882, AA195498, AA242878, AA242884, AA252152, AA251967, AA465181, AA465542, AA481105, AA481210, AA492206, AA732326
827503	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 2695 of SEQ ID NO:173, b is an integer of 15 to 2709, where both a	

	and b correspond to the positions of nucleotide residues shown in SEQ ID NO:173, and where b is greater than or equal to a + 14.	
827563	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 999 of SEQ ID NO:174, b is an integer of 15 to 1013, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:174, and where b is greater than or equal to a + 14.	
827565	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1683 of SEQ ID NO:175, b is an integer of 15 to 1697, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:175, and where b is greater than or equal to a + 14.	
827893	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1395 of SEQ ID NO:176, b is an integer of 15 to 1409, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:176, and where b is greater than or equal to a + 14.	
828072	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1489 of SEQ ID NO:177, b is an integer of 15 to 1503, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:177, and where b is greater than or equal to a + 14.	R20502, R45322, R45322, H29062, H29165, N36388, N39601, AA043930, AA044003, AA115568, AA115087, AA232982, AA234020, AA251431, AA251432, AA459761, AA768137, AA830696, AA918618, AA977409
828228	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1364 of SEQ ID NO:178, b is an integer of 15 to 1378, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:178, and where b is greater than or equal to a + 14.	T76992, T83862, R37649, R68086, R68125, H05325, H05379, H11520, H60866, N27826, N59149, N71661, AA004459, AA004512, AA026983, AA031653, AA045803, AA045870, AA127220, AA126199, AA129772, AA133788, AA131742, AA166788, AA216416, AA229513, AA469120, AA469189, AA503687, AA516488, AA522741, AA542827, AA614664, AA847108, AA876618, AA886579, AA887825, AA888263, AA888262, AA934459, N31217, D79619, N55800, AA026982, AA031743
828241	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 2237 of SEQ ID NO:179, b is an integer of 15 to 2251, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:179, and where b is greater than or equal to a + 14.	R09047, H71262, N28995, W07805, W89157, AA007537, AA203119

828287	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 986 of SEQ ID NO:180, b is an integer of 15 to 1000, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:180, and where b is greater than or equal to a + 14.	R00158, R34699, R34806, R55812, R55897, H02931, H04234, H38596, H38841, H38877, R84345, R84762, R85507, H51401, N22910, N31298, N36027, N64463, N70710, N80820, N94519, N99846, W15234, W15579, W15620, W23968, W24669, W30920, W31655, W37399, W37400, W39182, W45512, W44342, W45653, W44569, W44608, W47630, W47631, W52183, W52421, W57603, W58189, W58466, W60614, W73715, W78044, W90451, W90258, W92042, W91902, AA012954, AA013060, AA013459, AA013460, AA018132, AA018050, AA021226, AA021359, AA021556, AA021640, AA033802, AA040580, AA040552, AA047883, AA054092, AA055181, AA055893, AA082252, AA082502, AA099128, AA099165, AA100988, AA131285, AA136296, AA136178, AA151469, AA151470, AA156144, AA158033, AA158325, AA164422, AA164402, AA167105, AA182609, AA182541, AA187289, AA187406, AA523678, AA582094, AA570257, AA573999, AA574305, AA579097, AA661683, AA662869, AA664665, AA736798, AA770689, AA865267, AA902336, AA923648, AA933570, AA939196, AA988468, AI000226, AI089764, D79059, N84733, W73650, N86290, N88454, C04677, C06015, AA033803, R29541, AA089664, AA089996, C17096, C17255, C19033, AA093458
828364	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1415 of SEQ ID NO:181, b is an integer of 15 to 1429, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:181, and where b is greater than or equal to a + 14.	R55711, R55921, R68105, R68149, R72479, R72941, N70480, W72759
828371	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 2711 of SEQ ID NO:182, b is an integer of 15 to 2725, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:182, and where b is greater than or equal to a + 14.	T62048, T62112, T91683, T92364, T92416, T93284, N49690, N49793, N64329, N80813, W15549, W15404, W31643, W53039, W92220, W92342, AA055521, AA055520, AA149883, AA150063, AA148836, AA150436
828403	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1737 of SEQ ID NO:183, b is an integer of 15 to 1751, where both a	AA485171, AA515218, AA603721, AA612760, AA838541, AA970526, C18512

	and b correspond to the positions of nucleotide residues shown in SEQ ID NO:183, and where b is greater than or equal to a + 14.	
828501	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 2186 of SEQ ID NO:184, b is an integer of 15 to 2200, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:184, and where b is greater than or equal to a + 14.	H19145, N75547, AA044653, AA128979, AA159576, AA423963, AA523306, H62675, H97872, AA610503, AA010941, AA011327, AA043344
828520	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1973 of SEQ ID NO:185, b is an integer of 15 to 1987, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:185, and where b is greater than or equal to a + 14.	H70392, N30525, N30537, AA010769, AA463668, AA927343, AA091744
828527	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1723 of SEQ ID NO:186, b is an integer of 15 to 1737, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:186, and where b is greater than or equal to a + 14.	T39306, T40514, R08857, R08964, R00734, R00735, R13824, R20172, R37684, R44959, R44959, H05503, H17017, H17018, H54295, H54372, H54503, H67654, H67974, H87993, N33311, N37017, N44843, N55182, N75469, N75534, N77241, N93004, W05278, W05327, W45465, W88760, W88865, AA010623, AA010624, AA234956, AA235130, AA424457, AA282705, AA283023, AA283109, AA481529, AA481595, AA490727, AA491218, AA554176, AA614573, AA665370, AA687964, AA736921, AA765107, AA767430, AA809487, AA865595, N88052
828538	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1118 of SEQ ID NO:187, b is an integer of 15 to 1132, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:187, and where b is greater than or equal to a + 14.	
828541	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1253 of SEQ ID NO:188, b is an integer of 15 to 1267, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:188, and where b is greater than or equal to a + 14.	
828549	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 3773 of SEQ ID NO:189, b is an integer of 15 to 3787, where both a and b correspond to the positions of nucleotide	

	residues shown in SEQ ID NO:189, and where b is greater than or equal to a + 14.	
828562	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 540 of SEQ ID NO:190, b is an integer of 15 to 554, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:190, and where b is greater than or equal to a + 14.	
828576	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 860 of SEQ ID NO:191, b is an integer of 15 to 874, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:191, and where b is greater than or equal to a + 14.	
828602	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 2089 of SEQ ID NO:192, b is an integer of 15 to 2103, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:192, and where b is greater than or equal to a + 14.	
828628	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1303 of SEQ ID NO:193, b is an integer of 15 to 1317, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:193, and where b is greater than or equal to a + 14.	
828667	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1238 of SEQ ID NO:194, b is an integer of 15 to 1252, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:194, and where b is greater than or equal to a + 14.	
828684	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1674 of SEQ ID NO:195, b is an integer of 15 to 1688, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:195, and where b is greater than or equal to a + 14.	R11676, R12284, N68621, N71575, N99448, W02008, W58632, W74361, W76341, W78934, W85701, AA070898, AA070787, AA102636, AA102661, AA102678, AA190864, AA190957, AA197279, AA251577, AA464994, AA421724, AA470741, AA505341, AA506137, AA583780, AA579967, AA714136, AA743352, AA747903, AA814422, AA826755, AA836633, AA837944, AA936844, AI004160, C00265, AA641021
828727	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b,	R35925, R35954, R49443, R49468, R49443, R49468, N74960, AA083678, AA086366, AA100585, AA111863,

	where a is any integer between 1 to 742 of SEQ ID NO:196, b is an integer of 15 to 756, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:196, and where b is greater than or equal to a + 14.	AA156573, AA159175, AA192611, AA195925, AA195976, AA418567, AA418582
828734	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1457 of SEQ ID NO:197, b is an integer of 15 to 1471, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:197, and where b is greater than or equal to a + 14.	
828750	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 678 of SEQ ID NO:198, b is an integer of 15 to 692, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:198, and where b is greater than or equal to a + 14.	
828842	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1559 of SEQ ID NO:199, b is an integer of 15 to 1573, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:199, and where b is greater than or equal to a + 14.	R31695, R31737, R86919, R86763, H66952, N30849, N41376, N95538, W03782, W24227, N90171, AA020001, AA046039, AA046149, AA099753, AA489705, AA552582, AA580818, AA584291, AA730113, AA910268
828843	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 2728 of SEQ ID NO:200, b is an integer of 15 to 2742, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:200, and where b is greater than or equal to a + 14.	T57326, T57387, T94838, T94837, T94879, T94925, T74456, R11995, R15234, R19543, R21728, R36670, R39752, R39834, R40808, R40808, R43895, R70936, R70988, R74057, R74152, R79967, R80062, H02983, H04277, H08966, H09537, H25298, H25343, H25449, H25495, H29439, H29438, H29887, H29987, R86318, H65676, H87966, H88350, H97859, N20316, N26629, N27590, N39724, N52972, W39188, W45099, W45149, N90248, AA004834, AA033776, AA039900, AA039901, AA041524, AA044928, AA082729, AA085742, AA112974, AA128343, AA133157, AA171997, AA418609, AA418664, AA421626, AA430065, AA230107, AA230108, AA513630, AA521134, AA622056, AA635868, AA639882, AA714929, AA715480, AA715556, AA729814, AA731061, AA811597, AA830222, AA873240, AA886078, AA886270, AA907208, AA932201, AA977447, AA989000, D81476, N56281, C21262, AA089709
828851	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide	

	sequence described by the general formula of a-b, where a is any integer between 1 to 1403 of SEQ ID NO:201, b is an integer of 15 to 1417, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:201, and where b is greater than or equal to a + 14.	
828856	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1498 of SEQ ID NO:202, b is an integer of 15 to 1512, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:202, and where b is greater than or equal to a + 14.	
828862	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 405 of SEQ ID NO:203, b is an integer of 15 to 419, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:203, and where b is greater than or equal to a + 14.	AA021223
828870	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 2819 of SEQ ID NO:204, b is an integer of 15 to 2833, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:204, and where b is greater than or equal to a + 14.	
828873	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 5816 of SEQ ID NO:205, b is an integer of 15 to 5830, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:205, and where b is greater than or equal to a + 14.	
828892	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 741 of SEQ ID NO:206, b is an integer of 15 to 755, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:206, and where b is greater than or equal to a + 14.	R54649, W46198
828893	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1982 of SEQ ID NO:207, b is an integer of 15 to 1996, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:207, and where b is greater than or equal to a + 14.	
828897	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b,	

	where a is any integer between 1 to 1654 of SEQ ID NO:208, b is an integer of 15 to 1668, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:208, and where b is greater than or equal to a + 14.	
828910	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 2236 of SEQ ID NO:209, b is an integer of 15 to 2250, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:209, and where b is greater than or equal to a + 14.	T91595, T65436, T65518, T70584, T70847, T75377, R09159, R09261, R09950, T96365, T96446, R12590, R13068, R18120, R21193, R22430, R22480, R22810, R25025, R26742, R26976, R32026, R32079, R33017, R33904, R36588, R39200, R40499, R45972, R40499, R45972, R56330, R64494, R65591, R67446, R70974, R74477, R74579, R77932, R78301, R78497, R78547, R80142, R80143, H00643, H00729, H03024, H04306, H06614, H07124, H09643, H09677, H28706, H28835, H42802, H47310, R92010, H65658, H65657, H67068, H68151, H71685, H72248, H72786, H72785, H73342, H75583, H75514, H77433, H98557, N20087, N22979, N23822, N28617, N29593, N32509, N33262, N40705, N42724, N44752, N45195, N57760, N58105, N59101, N59726, N64423, N66868, N71993, N73995, N99375, W01801, W02025, W19280, W19667, W19930, W25451, W25645, W31475, W31938, W32153, W32005, W37711, W37710, W46758, W46905, W49818, W56089, W57771, W57844, W61375, W61376, W60415, W60416, W61142, W61190, W67942, W67941, W74649, W84332, W84393, W86146, W94323, AA016041, AA015933, AA022593, AA022594, AA030003, AA043309, AA069392, AA069393, AA069775, AA069812, AA102392, AA112674, AA112673, AA135337, AA135336, AA143448, AA152405, AA152459, AA149804, AA149829, AA149849, AA149856, AA156559, AA157731, AA159045, AA160734, AA173662, AA173661, AA235812, AA242974, AA243081, AA242998, AA252146, AA460003, AA460542, AA428205, AA429142, AA285041, AA283758, AA283993, AA480305, AA506566, AA524852, AA631324, AA575859, AA658502, AA766717, AA808234, AA837876, AA866075, AA877425, AA879058, AA886608, AA902179, AA904000, AA928667, AA937136, AA962263, AA995987, AI024986, W25995, W26229, W27231, W26246, W28106,

		W28807, W48809, C01974, AA640952, C14885, C15137
828927	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 824 of SEQ ID NO:210, b is an integer of 15 to 838, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:210, and where b is greater than or equal to a + 14.	
828932	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1199 of SEQ ID NO:211, b is an integer of 15 to 1213, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:211, and where b is greater than or equal to a + 14.	T50679, T51209, T78077, R42605, R48768, R42605, R91277, H61157, W38635, W44738, W46899, W80700, AA017684, AA017707, AA018069, AA019662, AA040254, AA053989, AA054041, AA070137, AA070138, AA074661, AA086354, AA158859, AA223111, AA224210, AA224315, AA232155, AA471047, AA588037, AA720832, AA872503
828933	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 955 of SEQ ID NO:212, b is an integer of 15 to 969, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:212, and where b is greater than or equal to a + 14.	
828941	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1680 of SEQ ID NO:213, b is an integer of 15 to 1694, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:213, and where b is greater than or equal to a + 14.	
828957	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1196 of SEQ ID NO:214, b is an integer of 15 to 1210, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:214, and where b is greater than or equal to a + 14.	R09987, R16645, R16734, R81727, H58067, H58066, H59815, H59816, H64860, H65458, N70923, W81647, W81187, AA052891, AA053046, AA251319, AA251723, AA262259, AA262870, AA463359, AA463865, AA417918, AA418169, AA480203, AA521273, AA836429, AA858135, AA888105, AA917914, AA937591, AA947712, AA961752, AA973797, AI085881
828963	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1762 of SEQ ID NO:215, b is an integer of 15 to 1776, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:215, and where b is greater than or equal to a + 14.	
828964	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide	

	sequence described by the general formula of a-b, where a is any integer between 1 to 1404 of SEQ ID NO:216, b is an integer of 15 to 1418, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:216, and where b is greater than or equal to a + 14.	
828966	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 2186 of SEQ ID NO:217, b is an integer of 15 to 2200, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:217, and where b is greater than or equal to a + 14.	T57322, T57383, R07432, R07433, R24183, R37889, R64196, R64212, H10798, H16281, H96182, N24864, N31801, N31897, N51466, N53607, N71323, N71374, N71696, N78973, N91801, N99595, N99806, W17338, W38617, W44695, W52815, W93325, W95029, AA027074, AA031625, AA031706, AA034522, AA101476, AA101477, AA156927, AA157179, AA173234, AA196758, AA506558, AA541561, AA552220, AA573198, AA687807, AA732065, AA769029, AA804914, AA858375, AA931935, AA995830, AI075078, AI075079, AA641307
828967	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1839 of SEQ ID NO:218, b is an integer of 15 to 1853, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:218, and where b is greater than or equal to a + 14.	T86194, T99270, R00981, R21065, R28076, R28291, R46245, R46245, R61751, R61752, H20415, H41325, H46347, H46354, W01107, W96450, W96548, AA082920, AA192528, AA494252, AA507548, AA604189, AA604361, AA614008, AA622126, AA573865, AA578191, AA568157, AA780392, AA812241, AA830010, AA836096, AA876742, C21216
828977	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1079 of SEQ ID NO:219, b is an integer of 15 to 1093, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:219, and where b is greater than or equal to a + 14.	T54853, T55018, T61617, T61701, T71718, T71787, R43855, R43855, H79047, W23509, W78022, AA028959, AA028960, AA035641, AA035749, AA040562, AA042827, AA044641, AA150059, AA459301, AA459532, AA419054, AA532924, AA603462, AA573839, AA863332, AA877269, AI016670, AI083871, AI085531
828978	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 2141 of SEQ ID NO:220, b is an integer of 15 to 2155, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:220, and where b is greater than or equal to a + 14.	
828979	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1250 of SEQ ID NO:221, b is an integer of 15 to 1264, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:221, and where b is greater than or equal to a + 14.	

829001	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 2071 of SEQ ID NO:222, b is an integer of 15 to 2085, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:222, and where b is greater than or equal to a + 14.	
829003	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 2907 of SEQ ID NO:223, b is an integer of 15 to 2921, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:223, and where b is greater than or equal to a + 14.	T56900, T56901, T57894, T57976, T58709, T83854, T83994, T83995, T85283, T85493, T85938, T98545, T98546, R23866, R51491, R51492, R70815, H06524, H06579, H21400, H22212, H26306, H26465, H40800, H42803, H44004, H45104, H45577, R84544. R85933, R95902, R98186, R98187, R99129, H51499, H62734, H62818, H67266, H67280, H67971, H72027, H72028, H86532, H86617, H97834, N22060, N22322, N22927, N23444, N23843, N27358, N27627, N31797, N53099, N55505, N55527, N62760, N76278, N76994, N81072, N99969, W07363, W15385, W30908, W32209, W32266, W37612, W39341, W45721, W44369, W60688, W60728, W74331, W79764, W79508, AA010902, AA011007, AA013382, AA013383, AA017180, AA018376, AA021435, AA128552, AA128295, AA161229, AA160487, AA236095, AA259037, AA458538, AA428449, AA491943, AA492101, AA501898, AA505736, AA551906, AA552335, AA554636, AA564579, AA588897, AA593936, AA595710, AA610733, AA612690, AA569349, AA570259, AA570263, AA573856, AA579746, AA658849, AA721609, AA743280, AA743326, AA808972, AA831035, AA836900, AA887420, AA887859, AA970292, AA994943, AA994947, AI014465, F19724, N36447, D78889, N75198, W37467, W79607, C03008, C04753
829016	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 4381 of SEQ ID NO:224, b is an integer of 15 to 4395, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:224, and where b is greater than or equal to a + 14.	
829027	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 3021 of SEQ ID	

	NO:225, b is an integer of 15 to 3035, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:225, and where b is greater than or equal to a + 14.	
829028	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1497 of SEQ ID NO:226, b is an integer of 15 to 1511, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:226, and where b is greater than or equal to a + 14.	
829031	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 2225 of SEQ ID NO:227, b is an integer of 15 to 2239, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:227, and where b is greater than or equal to a + 14.	T52373, T52446, T65540, T91789, R10959, T84998, R06717, R28502, R48288, R48390, R48442, R54616, R54879, R55311, R55316, R55413, R55418, R72602, R72669, R72946, H15595, H27333, H41543, H37781, R84976, R85050, R88513, R88514, H49052, H49116, H96219, H96754, H97979, N23664, N25056, N26150, N32997, N51857, N54122, W65281, W65277, W72409, W76488, W92510, N91031, AA045475, AA056943, AA057662, AA057806, AA126670, AA127032, AA136891, AA137001, AA158595, AA158989, AA279342, AA604130, AA604929, AA631863, C01812
829034	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 2332 of SEQ ID NO:228, b is an integer of 15 to 2346, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:228, and where b is greater than or equal to a + 14.	
829036	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 2232 of SEQ ID NO:229, b is an integer of 15 to 2246, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:229, and where b is greater than or equal to a + 14.	W19899, W56172, N91246, AA053015, AA258943, AA508101, AA557537, AA744258, C06034, AA053503
829049	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1988 of SEQ ID NO:230, b is an integer of 15 to 2002, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:230, and where b is greater than or equal to a + 14.	
829073	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 980 of SEQ ID	N71827, W07562, W79070, W94296, AA026190, AA215725, AA279902, AA832099

	NO:231, b is an integer of 15 to 994, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:231, and where b is greater than or equal to a + 14.	
829075	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 472 of SEQ ID NO:232, b is an integer of 15 to 486, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:232, and where b is greater than or equal to a + 14.	
829076	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 2067 of SEQ ID NO:233, b is an integer of 15 to 2081, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:233, and where b is greater than or equal to a + 14.	
829080	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 502 of SEQ ID NO:234, b is an integer of 15 to 516, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:234, and where b is greater than or equal to a + 14.	
829087	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1115 of SEQ ID NO:235, b is an integer of 15 to 1129, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:235, and where b is greater than or equal to a + 14.	
829092	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1031 of SEQ ID NO:236, b is an integer of 15 to 1045, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:236, and where b is greater than or equal to a + 14.	
829095	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 676 of SEQ ID NO:237, b is an integer of 15 to 690, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:237, and where b is greater than or equal to a + 14.	T98739, T98740, R53404, R72484, H09731, H16600, H21795, H25680, N79773, N93472, AA812105, AA826523, AA954170, AI084914
829096	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1859 of SEQ ID NO:238, b is an integer of 15 to 1873, where both a	T40001, T40939, R53257, R62981, R62980, R63036, H15127, H15187, H24078, H24188, H81472, H88927, H88927, H99390, N32032, N47835, N66666, N98950, AA022842,

	and b correspond to the positions of nucleotide residues shown in SEQ ID NO:238, and where b is greater than or equal to a + 14.	AA022965, AA024917, AA024918, AA035721, AA062907, AA102646, AA101299, AA223395, AA419511, AA421963, AA421964, AA524699, AA532380, AA614315, AA570194, AA742712, AA865440, AA887301, AA987486, AA988144, AA091175
829118	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 891 of SEQ ID NO:239, b is an integer of 15 to 905, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:239, and where b is greater than or equal to a + 14.	
829152	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1470 of SEQ ID NO:240, b is an integer of 15 to 1484, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:240, and where b is greater than or equal to a + 14.	T72498, T73568, T74363, T86984, R10378, R10477, T85969, R05924, R06022, H58205, H65999. H66000, N68870, N92084, N92944, AA188651, AA188754, N72345
829160	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1507 of SEQ ID NO:241, b is an integer of 15 to 1521, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:241, and where b is greater than or equal to a + 14.	R19077, R24890, R70937, R70989, R75822, R75823, H13581, R88030, H97197, H97205, H97610, H97622, H97640, H99011, N22163, N22211, N25706, N31618, N31627, N34096, N35586, N57066, N57078, N57083, N63961, N71248, N71530, N79638, W23686, W25345, W80523, W80524, AA027117, AA044025, AA044347, AA056543, AA056646, AA082122, AA120870, AA120871, AA129173, AA129197, AA173547, AA173713, AA190689, AA252595, AA258865, AA259007, AA576323, AA768606, N55993, N84224
829163	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1130 of SEQ ID NO:242, b is an integer of 15 to 1144, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:242, and where b is greater than or equal to a + 14.	R27150, H50951, N39917, N41848, N41877
829176	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 920 of SEQ ID NO:243, b is an integer of 15 to 934, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:243, and where b is greater than or equal to a + 14.	T46875, T53785, T62036, T73807, R11065, R11122, T84299, T85183, R01714, R02656, R02737, R02738, H41134, H64904, H79712, H79713, N68598, N71315, N71366, N99798, W01984
829204	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b,	R50489, R50573, R74498, R74499, AA234014, AA535362, AA554207, AA847239

	where a is any integer between 1 to 901 of SEQ ID NO:244, b is an integer of 15 to 915, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:244, and where b is greater than or equal to a + 14.	
829207	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1262 of SEQ ID NO:245, b is an integer of 15 to 1276, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:245, and where b is greater than or equal to a + 14.	
829228	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 3352 of SEQ ID NO:246, b is an integer of 15 to 3366, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:246, and where b is greater than or equal to a + 14.	T40764, T49773, T49774, H05098, H49148, H51985, H52105, N36154, N51490, N52526, N53635, AA054314, AA074167, AA152473, AA152472, AA188950, AA278366, AA281330, AA468930, AA469004, AA482010, AA542938, AA554491, AA565215, AA579406, AA741363, AA807139, AA832066, AA836995, AA876036, AA995854
829252	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 2134 of SEQ ID NO:247, b is an integer of 15 to 2148, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:247, and where b is greater than or equal to a + 14.	
829254	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 2211 of SEQ ID NO:248, b is an integer of 15 to 2225, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:248, and where b is greater than or equal to a + 14.	
829269	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1190 of SEQ ID NO:249, b is an integer of 15 to 1204, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:249, and where b is greater than or equal to a + 14.	
829277	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1300 of SEQ ID NO:250, b is an integer of 15 to 1314, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:250, and where b is greater than or equal to a + 14.	
829290	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide	

	sequence described by the general formula of a-b. where a is any integer between 1 to 1145 of SEQ ID NO:251, b is an integer of 15 to 1159, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:251, and where b is greater than or equal to a + 14.	
829294	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 2474 of SEQ ID NO:252, b is an integer of 15 to 2488, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:252, and where b is greater than or equal to a + 14.	
829299	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1540 of SEQ ID NO:253, b is an integer of 15 to 1554, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:253, and where b is greater than or equal to a + 14.	T82894, H25618, N48726, W52191, AA037331, AA223798, AA224330, AA635842, AA748884, AA826495, AA864458, AA903250, AA908466, AA931986, D81481, N56293, C02225
829308	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1492 of SEQ ID NO:254, b is an integer of 15 to 1506, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:254, and where b is greater than or equal to a + 14.	R13979, R17378, R40039, R42616, R42616, R40039, R56257, R56346, H05467, H07018, R86778, H99527, H99526, H99763, N24571, N25539, N25635, N28490, N30121, N34013, N34136, N34233, N35730, N49189, N50244, N92737, W20356, AA255602, AA262707, AA255576, AA262183, AA279758, AA570002, AA572777, AA721016, AA814424, AA864521, AA902860, AA948310, AI024777, AI056401
829349	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 640 of SEQ ID NO:255, b is an integer of 15 to 654, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:255, and where b is greater than or equal to a + 14.	T39288, T47082, T50451, T50586, T59000, T59073, T59535, T59586, T63704, T63861, T69920, T69974, T71240, T72474, T72943, T90268, T90710, T83786, T95048, R31368, R33435, R34369, R34489, R73911, R80467, R80667, R94351, R97310, R97345, H57329, H57376, H62783, H64845, H65444, H82981, H83214, H93955, H93956, N29780, N42940, N45379, N57200, N80805, W06876, W15396, W47162, W47283, W52164, W52024, W52758, W73045, W73275, W73604, W73643, W86783, W87274, AA009954, AA010849, AA011288, AA022621, AA022757, AA025805, AA025929, AA025968, AA046835, AA054475, AA058513, AA063327, AA075215, AA075451, AA088739, AA088740, AA099371, AA099457, AA112397, AA113053, AA121065, AA121066, AA132025, AA132147, AA132237, AA132357, AA146935,

		AA147721, AA147756, AA147602, AA148113, AA156063, AA157120, AA157223, AA157610, AA165107, AA164710, AA173741, AA173185, AA187331, AA187332, AA187293, AA187393, AA187741, AA188097, AA187033, AA188455, AA188457, AA188467, AA216356, AA228668, AA229001, AA228993, AA229108, AA397406, AA482922, AA483319, AA483431, AA491567, AA501502, AA507889, AA508445, AA513947, AA515053, AA522563, AA523140, AA525478, AA524922, AA526106, AA534088, AA535846, AA548219, AA552477, AA555012, AA558315, AA564882, AA565458, F16817, F16991, F17527, AA582793, AA587225, AA588487, AA595626, AA602055, AA602240, AA603392, AA631634, AA638971, AA639988, AA640535, AA576051, AA576894, AA566049, AA655021, AA659001, AA661609, AA662354, AA664631, AA664721, AA664980, AA665338, AA688035, AA714993, AA715012, AA720861, AA730373, AA730633, AA742678, AA742934, AA746812, AA747153, AA747192, AA747959, AA808437, AA836880, AA837645, AA838637, AA872341, AA876822, AA922665, AA961515, AA968734, AA970649, AA978219, AA988051, AA988404, AA991418, AA994111, AI002489, AI053409, AI053609, AI053760, AI082351, AI083631, N83854, N83948, N85971, N86260, N86628, N87758, AA641679, AA642097, AA642839, C20758, AA092159, AA092465, AA094493
829354	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1978 of SEQ ID NO:256, b is an integer of 15 to 1992, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:256, and where b is greater than or equal to a + 14.	
829388	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 2259 of SEQ ID NO:257, b is an integer of 15 to 2273, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:257, and where b is greater than or equal to a + 14.	
829540	Preferably excluded from the present invention are	N26408, N28830, N28838, N31522,

	one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1490 of SEQ ID NO:258, b is an integer of 15 to 1504, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:258, and where b is greater than or equal to a + 14.	W15157, W81560, W81561, AA126749, AA126756, AA126772, AA187148
829626	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1778 of SEQ ID NO:259, b is an integer of 15 to 1792, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:259, and where b is greater than or equal to a + 14.	
829730	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 2034 of SEQ ID NO:260, b is an integer of 15 to 2048, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:260, and where b is greater than or equal to a + 14.	
829892	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1268 of SEQ ID NO:261, b is an integer of 15 to 1282, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:261, and where b is greater than or equal to a + 14.	R84306, N99830, N90467, AA113938, AA192541, AA243317, L44546, AA713588
829933	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 585 of SEQ ID NO:262, b is an integer of 15 to 599, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:262, and where b is greater than or equal to a + 14.	AA121059, AA429187
829938	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1247 of SEQ ID NO:263, b is an integer of 15 to 1261, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:263, and where b is greater than or equal to a + 14.	AA001837, AA142857, AA235114, AA235222, AA614412, AA687460, AA857702, AA857893, AA962131, AA962521
829969	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1006 of SEQ ID NO:264, b is an integer of 15 to 1020, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:264, and where b is greater than or equal to a + 14.	R22931, R23036, H09755, H47088, N38971, N38985, N57545, AA075344, AA075597, AA136299, AA136180, AA279124, AA279243, AA279928, AA279929, AA909786, AI000293, N48117, N48131
829982	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide	H40097, N80803, N93871, W07650, W15482, W40363, W42635, W45238,

	sequence described by the general formula of a-b, where a is any integer between 1 to 557 of SEQ ID NO:265, b is an integer of 15 to 571, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:265, and where b is greater than or equal to a + 14.	W67482, W67483, W70331, W72456, W73235, W73290, W76515, W78220, AA040927, AA040928, AA074829, AA075095, AA083686, AA166708, AA167049, AA228843, AA468686, AA469044, AA505509, AA548788, AA564157, AA595572, AA622149, AA633298, AA576799, AA746697, AA807946, AA873193, AA903706, AA919114, AA932502, AA938506, AA974058, AA977996, AI000750, N85073, N86741, N87037, N88197, N88746, AA090569
830007	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1336 of SEQ ID NO:266, b is an integer of 15 to 1350, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:266, and where b is greater than or equal to a + 14.	
830019	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1305 of SEQ ID NO:267, b is an integer of 15 to 1319, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:267, and where b is greater than or equal to a + 14.	T61424, T53868, T61391, T63785, R23153, R23154, R23905, R64468, R65575, R69390, R69523, R79153, R79154, H14532, H14533, H47318, H47402, H53647, H61347, H93017, H94242, N29789, N42932, W57927, W58148, W67701, W68160, W74342, W81702, W81703, W94692, W95218, W95440, W95785, AA043712, AA056570, AA114073, AA133633, AA133634, AA151774, AA149729, AA149782, AA149795, AA425861, AA425990, AA428095, AA428642, AA494401, AA515475, AA523534, AA548827, AA552032, AA564916, F16977, AA593645, AA613557, AA617694, AA618542, AA576565, AA576574, AA746168, AA766359, AA833956, AA837906, AA857421, AA857877, AA903383, AA903849, AA903888, AA916517, AA922889, AA962544, AA970534, AA974964, AA975402, AA976089, AA983583, AA992448, F18477, C04429, C17306
830073	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 3680 of SEQ ID NO:268, b is an integer of 15 to 3694, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:268, and where b is greater than or equal to a + 14.	T93694, T96159, H04182, H04181, H15428, H48586, N74976, W05676, W44928, AA085826, AA085971, AA126446, AA425304, AA425408, AA280817, AA280995, AA287270, AA287417, AA668788, AA836455, AA977754
830130	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1228 of SEQ ID	

	NO:269, b is an integer of 15 to 1242, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:269, and where b is greater than or equal to a + 14.	
830134	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 2043 of SEQ ID NO:270, b is an integer of 15 to 2057, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:270, and where b is greater than or equal to a + 14.	
830135	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 946 of SEQ ID NO:271, b is an integer of 15 to 960, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:271, and where b is greater than or equal to a + 14.	
830148	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1153 of SEQ ID NO:272, b is an integer of 15 to 1167, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:272, and where b is greater than or equal to a + 14.	R15244, R31943, R31992, H06853, H06894, H13355, H30882, R84410, R84411, R94120, H53381, H97695, H99925, N46996, N69023, N77897, W00690, W19694, W38937, W74721, W74795, N89822, N89950, AA009490, AA009904, AA031349, AA031350, AA035629, AA035719, AA046140, AA062845, AA062905, AA079564, AA079636, AA116062, AA116046, AA126968, AA148568, AA159591, AA160429, AA161272, AA161273, AA160576, AA179774, AA180491, AA179635, AA182631, AA182727, AA179634, AA192371, AA192282, AA199831, AA251312, AA256883, AA255477, AA430121, AA533720, AA551694, AA552307, AA552661, AA582138, AA586611, AA587906, AA594387, AA602977, AA605299, AA633388, AA573941, AA574038, AA579715, AA687647, AA741352, AA838339, AA857603, AA858082, AA866081, AA865003, AA875861, AA910672, AA927563, AI076918, W21962
830149	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 2757 of SEQ ID NO:273, b is an integer of 15 to 2771, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:273, and where b is greater than or equal to a + 14.	R60249, R60762, R63751, R67526, H95029, H95095, N59347, N77158, W19778, AA047615, AA047555, AA047687, AA047738, AA056453, AA070880, AA112293, AA113105, AA112550, AA112614, AA158015, AA158228, AA160995, AA160996, AA190555, AA191131, AA224574, AA227422, AA255563, AA255586, AA418477, AA424689, AA470392, AA515485, AA515507, AA583475,

		AA588210, AA602533, AA573902, AA568354, AA746111, AA766146, AA804893, N83302
830154	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1875 of SEQ ID NO:274, b is an integer of 15 to 1889, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:274, and where b is greater than or equal to a + 14.	
830183	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 590 of SEQ ID NO:275, b is an integer of 15 to 604, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:275, and where b is greater than or equal to a + 14.	
830194	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1367 of SEQ ID NO:276, b is an integer of 15 to 1381, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:276, and where b is greater than or equal to a + 14.	T51023, T51115, T52795, T53595, T56300, T56767, T59691, T59827, T59904, T63354, T72200, T72269, T92900, T92990, R07165, R07217, R44334, R49609, R44334, R49609, H11106, H20800, H22618, H42472, H43453, H50320, H50321, H69947, N20118, N21306, N26128, N63140, N67225, N67232, W45407, W56419, W56420, W72419, W76279, W94626, W94710, AA029459, AA029524, AA034511, AA035053, AA035563, AA039819, AA041465, AA053002, AA055974, AA056002, AA070356, AA070320, AA074029, AA074039, AA074189, AA074336, AA075645, AA075646, AA076380, AA084435, AA084465, AA084453, AA085290, AA086454, AA099172, AA101922, AA101959, AA099618, AA102011, AA112794, AA126226, AA126304, AA128510, AA129955, AA133875, AA128443, AA133328, AA133403, AA134003, AA130990, AA131028, AA132940, AA135158, AA135628, AA143273, AA146730, AA151853, AA155641, AA155696, AA155726, AA157967, AA158903, AA158902, AA158943, AA158944, AA159293, AA159526, AA161206, AA160558, AA160739, AA160740, AA165357, AA167787, AA169218, AA169512, AA169691, AA176365, AA179272, AA179388, AA180903, AA181001, AA181325, AA181508, AA182781, AA173899, AA187757, AA188120, AA186725, AA187070, AA187152, AA190896, AA199819, AA223210,

		AA223254. AA227038. AA232399, AA233288. AA243192. AA252285, AA492525. AA420611, AA420688, AA492171. AA492254, AA503950, AA507398. AA513704, AA513757, AA515944, AA525799, AA558212, AA563863. AA565107, F17110, AA582829. AA586678. AA603895, AA604163, AA568617, AA617883, AA622814, AA635987, AA569079, AA570078, AA570258, AA570419, AA573205, AA573965, AA574048, AA566065. AA748781, AA834135, AA837022. AA838454. AA838636, AA838049. AA838058, AA856831, AA909853, AA910298, AA927706, AA932101. AA937900, AA953604, AA969555, AA973234, AA978074, AA985430, AA985432, AA988742, AA994207, AI002611, AI014411, N84537, N85082. W22113, W22114, W22431, W22639, W23207. W23271, W29046, N88675, AA640915, AA092777
830207	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1135 of SEQ ID NO:277, b is an integer of 15 to 1149, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:277, and where b is greater than or equal to a + 14.	R51744, R88177, W05323, AA746479, AA761644, AA826038, W27619, AA642452
830242	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 797 of SEQ ID NO:278, b is an integer of 15 to 811, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:278, and where b is greater than or equal to a + 14.	
830328	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1246 of SEQ ID NO:279, b is an integer of 15 to 1260, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:279, and where b is greater than or equal to a + 14.	
830340	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1654 of SEQ ID NO:280, b is an integer of 15 to 1668, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:280, and where b is greater than or equal to a + 14.	
830341	Preferably excluded from the present invention are	T62985, T63236, T71911, T66677,

	one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 2314 of SEQ ID NO:281, b is an integer of 15 to 2328, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:281, and where b is greater than or equal to a + 14.	T66678, T80777, T81178, R16218, R16219, R67281, H15642, H15643, R96139, R96356, H61487, H61952, H62021, H62022, H62510, H62577, H62887, H63016, H65659, H65660, H72388, H72834, H80906, H97768, N30162, N35776, N52509, N66853, W44421, AA004323, AA004410, AA025214, AA026003, AA040205, AA040849, AA079158, AA079159, AA137066, AA137080, AA137137, AA136971, AA193479, AA532656, AA602312, AA828635, AA872751, AA934418, D80729, C15337
830351	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 942 of SEQ ID NO:282, b is an integer of 15 to 956, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:282, and where b is greater than or equal to a + 14.	
830358	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1388 of SEQ ID NO:283, b is an integer of 15 to 1402, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:283, and where b is greater than or equal to a + 14.	
830390	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 661 of SEQ ID NO:284, b is an integer of 15 to 675, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:284, and where b is greater than or equal to a + 14.	
830400	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1325 of SEQ ID NO:285, b is an integer of 15 to 1339, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:285, and where b is greater than or equal to a + 14.	T40239, T41103, T60782, T61153, T92326, T95403, R16530, R16587, R46049, R49231, R49231, R46049, H26122, H26387, H67872, H67872, H97917, N23194, N29748, N57652, N64158, N67587, N77509, N80178, W03502, W23838, W57929, W72584, AA011087, AA011088, AA070667, AA074878, AA075068, AA075019, AA076166, AA079857, AA082235, AA099016, AA099093, AA100754, AA113152, AA126886, AA128207, AA126932, AA128546, AA130882, AA136302, AA136408, AA143052, AA143693, AA148079, AA149931, AA151001, AA151091, AA155761, AA157290, AA160781, AA165535, AA173281, AA179903, AA180211, AA181162, AA181673, AA181986,

		AA187551, AA191657, AA192202, AA196746, AA196944, AA223166, AA224485, AA242866, AA397377, AA468734, AA514807, AA523669, AA534165, AA534195, AA565551, AA565552, H67199, AA581627, AA588734, AA588752, AA593857, AA595407, AA595555, AA603965, AA610486, AA614617, AA631563, AA635960, AA636057, AA576256, AA577470, AA580124, AA580480, AA714208, AA728790, AA729276, AA729361, AA744895, AA745002, AA746940, AA746948, AA747346, AA804602, AA810873, AA833970, AA836938, AA838563, AA858405, AA872330, AA922975, AA946823, AA954185, AA962678, AA978008, AA985504, AA987717, AI004904, AI017374, AI075264, F19611, AI089951, N83301, AA082282, AA091465, AA093298, AA094459
830437	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1384 of SEQ ID NO:286, b is an integer of 15 to 1398, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:286, and where b is greater than or equal to a + 14.	
830458	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 912 of SEQ ID NO:287, b is an integer of 15 to 926, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:287, and where b is greater than or equal to a + 14.	T47583, T47584, T49761, T50148, T50203, T47161, R11382, R14878, H18220, H18258, R92715, N78687, W20222, W58210, W58319, W72115, W77801, W79332, W79431, W79487, W79631, W94437, N90582, AA043441, AA043442, AA148009, AA147947, AA150837, AA224863, AA225964, AA226110, AA259194, AA259193, AA420769, AA420829, AA470787, AA493672, AA501962, AA502082, AA506908, AA528607, AA588435, AA603500, AA603814, AA627229, AA627233, AA627240, AA632058, AA632689, AA639239, AA579023, AA580698, AA662633, AA661967, AA665215, AA729443, AA730546, AA737851, AA745424, AA745526, AA747036, AA878568, AA879157, AA886627, AA902180, AA922294, AA933050, AA962580, AA977360, AA985679, AA996058, AA996145, AI053546, AI085892, N83274, W15194, N88934, C04128, AA640839, AA091328, AA093116, AA094048, AA094287
830466	Preferably excluded from the present invention are	

	one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 3080 of SEQ ID NO:288, b is an integer of 15 to 3094, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:288, and where b is greater than or equal to a + 14.	
830497	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1969 of SEQ ID NO:289, b is an integer of 15 to 1983, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:289, and where b is greater than or equal to a + 14.	T47088, T47089, T58430, T58462, R00971, H42144, N77388, W51953, W52502, AA036671, AA114976, AA593693, AA575857, C01052
830511	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1284 of SEQ ID NO:290, b is an integer of 15 to 1298, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:290, and where b is greater than or equal to a + 14.	
830512	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 2445 of SEQ ID NO:291, b is an integer of 15 to 2459, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:291, and where b is greater than or equal to a + 14.	
830513	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 556 of SEQ ID NO:292, b is an integer of 15 to 570, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:292, and where b is greater than or equal to a + 14.	
830540	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 2454 of SEQ ID NO:293, b is an integer of 15 to 2468, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:293, and where b is greater than or equal to a + 14.	T66458, T98908, R15832, R21916, R22565, H12306, R99043, H57499, H82961, AA046203, AA046283, AA055081, AA055141, AA173411, AA173467, AA173996, AA176693
830550	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1066 of SEQ ID NO:294, b is an integer of 15 to 1080, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:294, and where b is greater than or equal to a + 14.	R50040, R60172, R71512, H09125, H09475, H21789, R84538, R85928, R94762, R96633, R96680, R97580, H53135, H53241, H82960, H83191, N68166, N68684, N77903, N80174, N80625, N92442, N93242, N93314, N98261, W03498, W05839, W20000, W25100, W31279, W37087, W60751, W67554, W67583, W73877, W77814, W80412, W95868, W95954, N91343,

		AA026891, AA026892, AA033547, AA034170, AA069175, AA088435, AA151307, AA161037, AA237097, AA251326, AA251729, AA428848, AA429940, AA287366, AA287504, AA470593, AA470594, AA514493, AA564438, H67293, AA582501, AA583172, AA587111, AA602517, AA603483, AA569955, AA732412, AA737913, AA810504, AA832193, AA857743, AA915872, AA915896, AA915992, AA948498, AA983538, AA991546, AI052409, AI053921
830567	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 2681 of SEQ ID NO:295, b is an integer of 15 to 2695, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:295, and where b is greater than or equal to a + 14.	R69708, R75813, R75814, N22294, N47088, N50300, N50983, N81194, N93236, AA074258, AA083867, AA083973, AA195801, AA196063, AA252500, AA252415, AA258014, AA287593, AA291332, AA492017, AA522597, AA617684, AA713960, AA740158, AA749386, AA808100, AA808680, AA814350, AA826203, AA831453, AA887306, AA918645, AA972761, N88184
830586	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1380 of SEQ ID NO:296, b is an integer of 15 to 1394, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:296, and where b is greater than or equal to a + 14.	R99131, H81094, W01508, AA045861, AA085947, AA102188, AA146772, AA148854, AA233843, AA424679, AA491204, AA514459, AA532818, AA809984, AA838521, AA954880, AI089939
830632	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 984 of SEQ ID NO:297, b is an integer of 15 to 998, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:297, and where b is greater than or equal to a + 14.	T47818, R21519, R21621, R22056, R22112, R31393, R32890, R48823, R48824, R66656, R67377, R71682, H25037, H25038, H25842, H26215, H26515, H26994, H28312, H28313, H29756, H30178, H41920, H41966, H42490, H43473, R83733, R85464, R88798, R89058, R93321, H52733, H59363, H60020, H73314, H73513, H80831, H80832, H82603, H86794, H86795, H86853, H86852, H92710, H96832, H98741, N23451, N23463, N26478, N26861, N31350, N31593, N35529, N39970, N42652, N62104, N74283, N76446, N78334, N92771, W04383, W19424, W20392, W24569, W35168, W60060, W60111, W84373, W84420, AA025658, AA029558, AA062705, AA062707, AA063390, AA062771, AA081934, AA126557, AA136019, AA151638, AA192245, AA194655, AA470430, AA493634, AA552261, AA552348, AA565278, AA565462, AA583788, AA593646, AA594277, AA604853, AA613755,

		AA632449, AA632505, AA657974, AA730677, AA730804, AA748100, AA765824, AA857805, AA954102, AA961763, AA962500, AA974525, AA983564, AA987422, AA987934, AA989423, AI000235, F19140, N84058, N84994, C03222, AA091370, AA091545
830645	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1652 of SEQ ID NO:298, b is an integer of 15 to 1666, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:298, and where b is greater than or equal to a + 14.	
830652	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 2430 of SEQ ID NO:299, b is an integer of 15 to 2444, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:299, and where b is greater than or equal to a + 14.	
830659	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1012 of SEQ ID NO:300, b is an integer of 15 to 1026, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:300, and where b is greater than or equal to a + 14.	T65101, T66494, T66636, T84051, T86086, R05580, R13805, R15868, R16050, H05221, H05222, H13512, H16069, H18275, H21247, H44169, R83705, R92365, H48479, H48643, H54436, H54526, H73472, H73726, H97495, N29822, N30479, N31551, N32563, N39176, N39961, N45251, N68667, N91684, W07693, W32510, W32607, W38017, W74179, W79849, AA018138, AA028191, AA033572, AA033571, AA042915, AA043002, AA053878, AA054501, AA058344, AA099556, AA101993, AA134643, AA143525, AA176419, AA424269, AA555196, AA769107, AA987653, AI076212, N84624, N85006, AI084132, AI084154, AA094327
830696	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 816 of SEQ ID NO:301, b is an integer of 15 to 830, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:301, and where b is greater than or equal to a + 14.	
830706	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 3286 of SEQ ID NO:302, b is an integer of 15 to 3300, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:302, and where b is	

	greater than or equal to a + 14.	
830743	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 461 of SEQ ID NO:303, b is an integer of 15 to 475, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:303, and where b is greater than or equal to a + 14.	N30323, N56655, N69079, N69946, N80244, N98327, W07371, W42660, W45185, W55989, W56279, W68387, W68503, W72685, W74708, W74677, W77791, W80647, AA010723, AA011171, AA033537, AA034221, AA035773, AA056334, AA062820, AA132021, AA132124, AA135594, AA135681, AA151293, AA151292, AA181331, AA186392, AA187084, AA228662, AA228680, AA229819, AA468802, AA470869, AA483684, AA491891, AA514852, AA533423, AA548946, AA563674, AA564612, AA594511, AA600707, AA622053, AA635767, AA639353, AA662887, AA664589, AA729365, AA747035, AA747774, AA814124, AA873167, AA886626, AA903495, AA903981, AA922807, AA969768, AA973174, AA974282, AA976458, AA977143, AA983332, AI025140, AI066527, F19035, F19464, C03984, C13986, C14221, C14299, C14336, C14341, C14380, C14385, C14396, C14434, C14483, C14504, C14513, C15788
830770	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 2888 of SEQ ID NO:304, b is an integer of 15 to 2902, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:304, and where b is greater than or equal to a + 14.	
830830	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1539 of SEQ ID NO:305, b is an integer of 15 to 1553, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:305, and where b is greater than or equal to a + 14.	
830838	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1973 of SEQ ID NO:306, b is an integer of 15 to 1987, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:306, and where b is greater than or equal to a + 14.	
830851	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 771 of SEQ ID NO:307, b is an integer of 15 to 785, where both a and b correspond to the positions of nucleotide	

	residues shown in SEQ ID NO:307. and where b is greater than or equal to a + 14.	
830853	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 2164 of SEQ ID NO:308, b is an integer of 15 to 2178, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:308, and where b is greater than or equal to a + 14.	
830856	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 861 of SEQ ID NO:309, b is an integer of 15 to 875, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:309, and where b is greater than or equal to a + 14.	
830862	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 742 of SEQ ID NO:310, b is an integer of 15 to 756, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:310, and where b is greater than or equal to a + 14.	T46908, T46909, T46921, T46922, T50921, T52918, T53038, T56001, T59028, T94115, T94204, R53898, R53908, H02747, H27523, H77792, H88026, H88248, H90255, H96065, H88248, N21994, N64072, N73723, N74262, N75815, N77939, W03894, W23887, AA081082, AA113423, AA115852, AA143290, AA143335, AA146868, AA157054, AA157208, AA179118, AA187792, AA188385, AA468513, AA468983, AA501970, AA523481, AA528461, AA533759, AA533618, AA535287, AA541570, AA558529, L44430, AA604961, AA568927, AA659814, AA661481, AA661996, AA731036, AA748135, AA847331, AA878667, AA885549, AA935403, AA938035, AI001062, F19242, N83489, N83646, N84328, N85002, N85167, N85223, N85325, N85833, N85949, N86287, N86329, N87923, N83150, AA642852, AA091775, AA093919
830879	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 837 of SEQ ID NO:311, b is an integer of 15 to 851, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:311, and where b is greater than or equal to a + 14.	T62074, T62130, T67747, T67857, R44816, R48904, R44816, H13822, H29311, W37451, N90567, AA128266, AA164552, AA235044, AA236012, AA746229, AA962194, AA987868, AA994828, AI000188, AI015557
830919	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1321 of SEQ ID NO:312, b is an integer of 15 to 1335, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:312, and where b is	

	greater than or equal to a + 14.	
830969	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 502 of SEQ ID NO:313, b is an integer of 15 to 516, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:313, and where b is greater than or equal to a + 14.	
830991	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1819 of SEQ ID NO:314, b is an integer of 15 to 1833, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:314, and where b is greater than or equal to a + 14.	
831002	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1340 of SEQ ID NO:315, b is an integer of 15 to 1354, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:315, and where b is greater than or equal to a + 14.	
831003	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 2407 of SEQ ID NO:316, b is an integer of 15 to 2421, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:316, and where b is greater than or equal to a + 14.	T64373, N48387, W52748, W52754, W70187, AA029541, AA034463, AA058497, AA082001, AA082284, AA085967, AA088397, AA133444, AA133477, AA149568, AA187408, AA226818, AA226855
831021	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1078 of SEQ ID NO:317, b is an integer of 15 to 1092, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:317, and where b is greater than or equal to a + 14.	
831036	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1366 of SEQ ID NO:318, b is an integer of 15 to 1380, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:318, and where b is greater than or equal to a + 14.	
831071	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 2598 of SEQ ID NO:319, b is an integer of 15 to 2612, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:319, and where b is greater than or equal to a + 14.	

831094	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 929 of SEQ ID NO:320, b is an integer of 15 to 943, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:320, and where b is greater than or equal to a + 14.	
831099	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 2945 of SEQ ID NO:321, b is an integer of 15 to 2959, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:321, and where b is greater than or equal to a + 14.	T58120, T90056, T90158, T94290, T94639, R69200, R69590, R69678, R76031, H65424, H65425, N32273, N40465, N47619, N48504, N66482, N67212, N67243, N67881, N71915, N72302, N92538, N94512, W03004, W06930, W20370, W23962, W38380, W38525, W38716, W39486, W42582, W42594, W44824, W48665, W51898, W52474, W53040, W60142, N90075, N90423, AA025009, AA024962, AA029382, AA029726, AA031500, AA031546, AA037283, AA037749, AA039259, AA044145, AA044261, AA065061, AA070027, AA082386, AA083544, AA083757, AA088692, AA088829, AA099577, AA100236, AA100245, AA100517, AA112739, AA112091, AA116055, AA130509, AA130510, AA132145, AA135909, AA136308, AA136413, AA136528, AA136751, AA146853, AA146852, AA148049, AA156943, AA159808, AA165022, AA173867, AA181803, AA182563, AA182776, AA186553, AA186858, AA192463, AA194658, AA255837, AA261995, AA423999, AA493599, AA228337, AA228348, AA506755, AA506420, AA513968, AA514542, AA522900, AA524125, AA551485, AA553912, AA563900, AA594966, AA602651, AA610339, AA610361, AA614772, AA618333, AA576828, AA665045, AA714493, AA729997, AA738153, AA768641, AA804931, AA806122, AA827914, AA857664, AA876216, AA877173, AA877646, AA894385, AA922728, AA947835, AA977110, AA984009, AA988275, AA988567, N84005, N84600, N84939, N85553, A1084028, N86141, N88049, N89450, N89451, C02877, C02980, C03631, C05243, C05332, C05993, AA642453, AA090838, AA089614, AA091652, AA093130, AA093851
831113	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b,	AA122085, AA147371, A1005336

	where a is any integer between 1 to 788 of SEQ ID NO:322, b is an integer of 15 to 802, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:322, and where b is greater than or equal to a + 14.	
831120	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1710 of SEQ ID NO:323, b is an integer of 15 to 1724, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:323, and where b is greater than or equal to a + 14.	
831172	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 2247 of SEQ ID NO:324, b is an integer of 15 to 2261, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:324, and where b is greater than or equal to a + 14.	
831178	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1199 of SEQ ID NO:325, b is an integer of 15 to 1213, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:325, and where b is greater than or equal to a + 14.	
831184	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 2750 of SEQ ID NO:326, b is an integer of 15 to 2764, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:326, and where b is greater than or equal to a + 14.	
831203	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1750 of SEQ ID NO:327, b is an integer of 15 to 1764, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:327, and where b is greater than or equal to a + 14.	
831210	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 557 of SEQ ID NO:328, b is an integer of 15 to 571, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:328, and where b is greater than or equal to a + 14.	AA057014, AA059289
831228	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 459 of SEQ ID	

	NO:329, b is an integer of 15 to 473, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:329, and where b is greater than or equal to a + 14.	
831256	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1321 of SEQ ID NO:330, b is an integer of 15 to 1335, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:330, and where b is greater than or equal to a + 14.	R17500, R48877, H12160, R84358, H90367, N33987, AA161057
831257	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1032 of SEQ ID NO:331, b is an integer of 15 to 1046, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:331, and where b is greater than or equal to a + 14.	T49922, T85470, R37545, H03610, AA005184, AA045346
831277	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1297 of SEQ ID NO:332, b is an integer of 15 to 1311, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:332, and where b is greater than or equal to a + 14.	
831317	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1430 of SEQ ID NO:333, b is an integer of 15 to 1444, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:333, and where b is greater than or equal to a + 14.	T39850, T47708, T47709, T47863, T51491, T52507, T53819, T53951, T55884, T60330, T60359, T60364, T60380, T60480, T60634, T61198, T61280, T61878, T62028, T67704, T67742, T67780, T67853, T67910, T68010, T68058, T68132, T68154, T68379, T68998, T68999, T69078, T69079, T69119, T69177, T69442, T70496, T71707, T72285, T72505, T72998, T73123, T73679, T73756, T73761, T73837, T74031, T74383, T74405, T74655, T74784, T74798, T74892, T85320, T85533, R83453, R88738, R90989, R90995, H58528, H59441, H60092, H60282, H60589, H67401, H67458, H72811, H79422, H80518, H80570, H91775, H91816, N57814, W60714, W60741, AA034367, AA040550, AA040667, AA242768, AA424551, AA424642, R29495, R29660, R29089, C21224
831339	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1016 of SEQ ID NO:334, b is an integer of 15 to 1030, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:334, and where b is	

	greater than or equal to a + 14.	
831363	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 2113 of SEQ ID NO:335, b is an integer of 15 to 2127, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:335, and where b is greater than or equal to a + 14.	T58736, T58803, T61766, T64470, T64610, T67816, T68878, T68952, T72450, T72511, T72968, T73613, T73939, H41914, H41957, N75040, W05718, AA043436, AA043416, AA045231, AA058807, AA484773, AA502762, AA503811, AA527553, AA744171, AA902935, AA903099, AI002033
831367	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 833 of SEQ ID NO:336, b is an integer of 15 to 847, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:336, and where b is greater than or equal to a + 14.	
831379	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 688 of SEQ ID NO:337, b is an integer of 15 to 702, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:337, and where b is greater than or equal to a + 14.	R26001, R26804, R82629, R82630, H21598, H27310, H27309, H38082, H38083, H44451, H44494, H47613, R83356, R83791, R96066, R96103, H72512, H72910, H80449, H80450, H90511, H90607, N71766, N94349, W16956, W23496, W24351, W46455, W46523, W48658, W70263, W73002, W76239, W92963, W92964, AA157329, AA157426, AA458665, AA229554, AA280810, AA280936, AA490898, AA491084, AA493730, AA527336, AA534762, AA535794, F17720, AA603439, AA568655, AA659071, AA826699, AA872867, AA876999, AA932403, AA953149, AA953343, AI000023, AI017353, AI094807, N95548, C02063, C04109
831385	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 861 of SEQ ID NO:338, b is an integer of 15 to 875, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:338, and where b is greater than or equal to a + 14.	
831390	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1434 of SEQ ID NO:339, b is an integer of 15 to 1448, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:339, and where b is greater than or equal to a + 14.	T53890, T54037, T81546, T81973, R20470, R21066, R45288, R46246, R45288, R46246, H13340, H17537, H30523, R85229, R85230, R94643, R94685, R94686, H52010, H52125, H71328, H71376, N25973, N28794, N30891, N36603, N41703, N62205, N63213, N76503, W45706, W44353, W52126, W74523, W79862, AA033566, AA034468, AA099015, AA099092, AA100315, AA129588, AA167137, AA194961, AA226935, AA226943, AA418898, AA428909,

		AA485083, AA485195, AA505107, AA506087, AA516109, AA525370, AA617946, AA627402, AA573848, AA574063, AA809830, AA834509, AA837985, AA862394, AA862989, AA974789, AA988779, AI000171, AI094917, W24010, N88026, C20972
831391	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 829 of SEQ ID NO:340, b is an integer of 15 to 843, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:340, and where b is greater than or equal to a + 14.	
831405	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1279 of SEQ ID NO:341, b is an integer of 15 to 1293, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:341, and where b is greater than or equal to a + 14.	T54632, T54714, T55384, T55812, T56220, T60613, T69578, R08164, R08219, T78003, T78164, R01577, R12676, R16414, H60551, N21984, N25878, N25887, N75352, W01648, W72541, W76166, W86984, W86811, W88909, W88788, AA022691, AA022784, AA193302, AA194256, AA235873, AA425660, AA573463, AA953249, R29055
831442	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1259 of SEQ ID NO:342, b is an integer of 15 to 1273, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:342, and where b is greater than or equal to a + 14.	
831476	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1779 of SEQ ID NO:343, b is an integer of 15 to 1793, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:343, and where b is greater than or equal to a + 14.	R48303, R48405, R73778, H30456, H81254, W02773, W24831, W73089, W73194, AA034015, AA151153, AA151154, AA418429, AA424672, AA593592, AA910532, AA987246, AI001017, C02335, C04320
831488	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1658 of SEQ ID NO:344, b is an integer of 15 to 1672, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:344, and where b is greater than or equal to a + 14.	
831518	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 2095 of SEQ ID NO:345, b is an integer of 15 to 2109, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:345, and where b is greater than or equal to a + 14.	

831519	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1700 of SEQ ID NO:346, b is an integer of 15 to 1714, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:346, and where b is greater than or equal to a + 14.	
831521	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1658 of SEQ ID NO:347, b is an integer of 15 to 1672, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:347, and where b is greater than or equal to a + 14.	
831550	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1469 of SEQ ID NO:348, b is an integer of 15 to 1483, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:348, and where b is greater than or equal to a + 14.	
831560	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1828 of SEQ ID NO:349, b is an integer of 15 to 1842, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:349, and where b is greater than or equal to a + 14.	T56438, R22852, R46063, R52365, R81781, R81879, H02958, H04256, H05743, H05849, H23235, H23349, H43210, H43260, H87699, H91571, W00708, W56717, W56762, W70251, W70252, AA026841, AA027043, AA041261, AA041495, AA043451, AA043452, AA054505, AA054366, AA055050, AA055129, AA147629, AA147667
831562	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 2994 of SEQ ID NO:350, b is an integer of 15 to 3008, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:350, and where b is greater than or equal to a + 14.	
831570	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 2742 of SEQ ID NO:351, b is an integer of 15 to 2756, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:351, and where b is greater than or equal to a + 14.	
831593	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1631 of SEQ ID NO:352, b is an integer of 15 to 1645, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:352, and where b is	

	greater than or equal to a + 14.	
831596	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1623 of SEQ ID NO:353, b is an integer of 15 to 1637, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:353, and where b is greater than or equal to a + 14.	
831627	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1105 of SEQ ID NO:354, b is an integer of 15 to 1119, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:354, and where b is greater than or equal to a + 14.	AA147578, AA156449, AA588796, AA863066, D80116
831649	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 724 of SEQ ID NO:355, b is an integer of 15 to 738, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:355, and where b is greater than or equal to a + 14.	R21047
831664	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1952 of SEQ ID NO:356, b is an integer of 15 to 1966, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:356, and where b is greater than or equal to a + 14.	R35205, H13039, R84255, W24589, W93157, AA186436, AA188774, AA227246, AA658889, AA838204, W22056, W25833, W28198, W28494, AA090436, AA089530, AA089667
831674	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1548 of SEQ ID NO:357, b is an integer of 15 to 1562, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:357, and where b is greater than or equal to a + 14.	
831684	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1917 of SEQ ID NO:358, b is an integer of 15 to 1931, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:358, and where b is greater than or equal to a + 14.	T64083, R54664, R54665, W52888, W60096, W60162, AA009843, AA009870, AA236225, AA236291, AA459452, AA465675, AA554776, AA563899, AA583755, AA593849, AA596013, AA627978, AA573921, AA747840, AA828086, AA830260, AA837593, AA996154, C01662
831687	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 855 of SEQ ID NO:359, b is an integer of 15 to 869, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:359, and where b is greater than or equal to a + 14.	T49489, R05976, R55046, N21648, N31054, N48001, AA464953, AA426224, AA430556, AA600829, AA744708, AA747361, AA976473, A1097658

831726	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 547 of SEQ ID NO:360, b is an integer of 15 to 561, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:360, and where b is greater than or equal to a + 14.	
831736	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1666 of SEQ ID NO:361, b is an integer of 15 to 1680, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:361, and where b is greater than or equal to a + 14.	T60384, T93026, T83297, R17403, R17423, R21319, H65765, N94506, W23956, W24344, W45068, W57786, W57860, W81343, AA058929, AA151788, AA151833
831762	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 726 of SEQ ID NO:362, b is an integer of 15 to 740, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:362, and where b is greater than or equal to a + 14.	
831801	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1310 of SEQ ID NO:363, b is an integer of 15 to 1324, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:363, and where b is greater than or equal to a + 14.	T39530, T64430, R36089, H12597, H12647, H19534, H20096, H26648, H26663, W15192, W45569, W45621, AA018144, AA018145, AA018470, AA039510, AA039529, AA047549, AA047837, AA057785, AA074201, AA075686, AA079138, AA135599, AA135658, AA147502, AA147931, AA156715, AA156811, AA188215, AA186362, AA425996, AA283917, AA514670, AA522463, AA714301, AA742700, AA872728, AA887841, AA971644, AI015637, AI053971, AI054233, AI074507, AI084901, W28363
831848	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 2839 of SEQ ID NO:364, b is an integer of 15 to 2853, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:364, and where b is greater than or equal to a + 14.	T77112, R13655, R19353, R19511, R24780, R35812, R36752, R38177, R43861, R44629, R45511, R43861, R45511, R44629, R71248, R71299, R82784, H00629, H01917, H04479, H45706, H45757, H94039, H94125, N30574, N57220, AA033684, AA114107, AA253260, AA461547, AA460619, AA715125, AI096588, C03714, AA092127
831861	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1823 of SEQ ID NO:365, b is an integer of 15 to 1837, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:365, and where b is greater than or equal to a + 14.	T57456, T58038, T58104, R08156, R27046, R28341, R28340, N32411, N56831, N78961, W16984, W16954, W17352, W74522, W79861, AA025882, AA025883, AA084109, AA100121, AA100060, AA132713

831866	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1809 of SEQ ID NO:366, b is an integer of 15 to 1823, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:366, and where b is greater than or equal to a + 14.	
831878	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 884 of SEQ ID NO:367, b is an integer of 15 to 898, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:367, and where b is greater than or equal to a + 14.	
831899	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1103 of SEQ ID NO:368, b is an integer of 15 to 1117, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:368, and where b is greater than or equal to a + 14.	AA159048, AA768390, AA806956
831913	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 2212 of SEQ ID NO:369, b is an integer of 15 to 2226, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:369, and where b is greater than or equal to a + 14.	
831972	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 3622 of SEQ ID NO:370, b is an integer of 15 to 3636, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:370, and where b is greater than or equal to a + 14.	
831985	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 4025 of SEQ ID NO:371, b is an integer of 15 to 4039, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:371, and where b is greater than or equal to a + 14.	
831986	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1585 of SEQ ID NO:372, b is an integer of 15 to 1599, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:372, and where b is greater than or equal to a + 14.	
832010	Preferably excluded from the present invention are	

	one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 450 of SEQ ID NO:373, b is an integer of 15 to 464, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:373, and where b is greater than or equal to a + 14.	
832016	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 876 of SEQ ID NO:374, b is an integer of 15 to 890, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:374, and where b is greater than or equal to a + 14.	
832041	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1860 of SEQ ID NO:375, b is an integer of 15 to 1874, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:375, and where b is greater than or equal to a + 14.	R63637, R92994, N30838, N30844, N41366, N41372, AA639771
832044	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 2004 of SEQ ID NO:376, b is an integer of 15 to 2018, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:376, and where b is greater than or equal to a + 14.	T56668, R09616, R20197, R44983, R52998, R52997, R44983, H06485, H06543, H09799, H09885, H24790, N57987, N62197, N76494, W02915, W78217, AA041290, AA041323, AA074236, AA075127, AA075212, AA075847, AA088708, AA088793, AA112359, AA121803, AA151677, AA166711, AA167069, AA181608, AA188478, AA194067, AA194182, AA221025, AA221037, AA228036, AA228145, AA557397, AA564567, AA582681, AA582151, AA601549, AA613841, AA832393, AA846987, AA865356, AA866164, AA872667, AA862962, AA911092, AA937359, AI000072, D83877
832049	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 804 of SEQ ID NO:377, b is an integer of 15 to 818, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:377, and where b is greater than or equal to a + 14.	
832122	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 2551 of SEQ ID NO:378, b is an integer of 15 to 2565, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:378, and where b is greater than or equal to a + 14.	
832148	Preferably excluded from the present invention are	T78202, R37864, R62706, R78737,

	one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1666 of SEQ ID NO:379, b is an integer of 15 to 1680, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:379, and where b is greater than or equal to a + 14.	R78736, H62109, N50394, N51659, N67973, N80394, W33108, W33107, AA016055, AA074831, AA075097, AA256793, AA256472, AA418825, AA418922, AA430755, AA280663, AA281049, AA467867, AA502148, H71558, AA721278, AA748880, AA809767, AA810852, AA832174, AA911263, AA938484, AA975282, D80672, D81573, D81746, AI096900, C02375
832197	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1253 of SEQ ID NO:380, b is an integer of 15 to 1267, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:380, and where b is greater than or equal to a + 14.	
832237	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1017 of SEQ ID NO:381, b is an integer of 15 to 1031, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:381, and where b is greater than or equal to a + 14.	R36943, R42259, R53230, R42259, H09607, AA150724, AA831055
832246	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1583 of SEQ ID NO:382, b is an integer of 15 to 1597, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:382, and where b is greater than or equal to a + 14.	H13698, H13750, R91283, R91322, H97506, N64810, N75659, W61290, W65386, H54890, AA568261, AA830860, AA863239, AA873329, AA938701, D82264, C18047
832256	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 161 of SEQ ID NO:383, b is an integer of 15 to 175, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:383, and where b is greater than or equal to a + 14.	
832280	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 2157 of SEQ ID NO:384, b is an integer of 15 to 2171, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:384, and where b is greater than or equal to a + 14.	H09977, H09978, R89392, R94438, H93033, H93466, H93904, N29334, N53767, N57027, N71868, N71879, N73126, W24652, AA026682, AA047124, AA127259, AA224396, AA224473, AA227220, AA236734, AA236763, AA236910, AA236919
832285	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 2350 of SEQ ID NO:385, b is an integer of 15 to 2364, where both a and b correspond to the positions of nucleotide	R12740, R14184, R15171, R26447, R28455, R34165, R35396, R39792, R40473, R49696, R41588, R40473, R49696, R70668, R70669, R79640, R79833, H02312, H08199, H08297, R99351, H84241, H84567, H85554,

	residues shown in SEQ ID NO:385, and where b is greater than or equal to a + 14.	N24354, N25230, N32462, N33863, N64676, N70374, N80109, W47526, W47527, W80678, W80934, W93668, AA082195, AA223758, AA243624, AA255527, AA256711, AA262387, AA281015, AA281094, AA281183, AA281203, AA287927, AA287991, AA505084, AA505086, AA525301, AA553559, AA564243, AA582189, AA737010, AA808271, AA872481, AA937541, AI015987, C01015, C20842
832294	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 2850 of SEQ ID NO:386, b is an integer of 15 to 2864, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:386, and where b is greater than or equal to a + 14.	
832326	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 2669 of SEQ ID NO:387, b is an integer of 15 to 2683, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:387, and where b is greater than or equal to a + 14.	
832333	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1432 of SEQ ID NO:388, b is an integer of 15 to 1446, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:388, and where b is greater than or equal to a + 14.	
832346	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 709 of SEQ ID NO:389, b is an integer of 15 to 723, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:389, and where b is greater than or equal to a + 14.	T88928, R12446, R37113, R42462, H15692, H18859, N34664, AA132220, AA224337, AA460720, AA492479
832370	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1032 of SEQ ID NO:390, b is an integer of 15 to 1046, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:390, and where b is greater than or equal to a + 14.	
832381	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 685 of SEQ ID NO:391, b is an integer of 15 to 699, where both a	

	and b correspond to the positions of nucleotide residues shown in SEQ ID NO:391, and where b is greater than or equal to a + 14.	
832394	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1531 of SEQ ID NO:392, b is an integer of 15 to 1545, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:392, and where b is greater than or equal to a + 14.	
832454	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 735 of SEQ ID NO:393, b is an integer of 15 to 749, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:393, and where b is greater than or equal to a + 14.	T57094, T58711, T68990, T71879, R92183, H93778, N63977, N80768, AA034382, AA034383, AA057664, AA235744, AA425865, AA524693, AA551804, AA523604, AA614639, AA740316, AA872373, AA938571, AA947337, R28997, AA640968, C21135
832465	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 597 of SEQ ID NO:394, b is an integer of 15 to 611, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:394, and where b is greater than or equal to a + 14.	R36004, R36378, H71881, H96279, N50049, N63692, W74426, W79180, W87805, AA421015, AA527679, AA833773, AA987375, F19351, AA642491, C14893, C14937
832475	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1842 of SEQ ID NO:395, b is an integer of 15 to 1856, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:395, and where b is greater than or equal to a + 14.	
832495	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 2637 of SEQ ID NO:396, b is an integer of 15 to 2651, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:396, and where b is greater than or equal to a + 14.	
832498	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 2493 of SEQ ID NO:397, b is an integer of 15 to 2507, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:397, and where b is greater than or equal to a + 14.	T67126, T67127, R13516, R20638, H64071, N22361, N25516, N39506, N75609, N78204, W40313, W45344, AA074739, AA074803, AA143509, AA523999, AA552542, AA554032, N20483, AA588804, AA617733, AA577150, AA577309, AA579423, AA740813, AA835721, AA836640, AA909766, AA936979, AA947310, N26815, AI085484, D78707, W67520, W68152
832501	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b,	

	where a is any integer between 1 to 1259 of SEQ ID NO:398, b is an integer of 15 to 1273, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:398, and where b is greater than or equal to a + 14.	
832505	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 3760 of SEQ ID NO:399, b is an integer of 15 to 3774, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:399, and where b is greater than or equal to a + 14.	T50501, T50636, T92136, R52390, R59648, H06170, H28886, H28885, R96577, R96600, H84171, H94122, H98228, N36866, N36872, N46136, N46142, N63589, N66323, W48779, W49798, AA029033, AA054487, AA058524, AA084466, AA086177, AA098967, AA099485, AA100345, AA147008, AA147009, AA146910, AA146909, AA160346, AA159865, AA192832, AA203513, AA252521, AA252553, AA463513, AA463570, AA421250, AA425704, AA427774, AA278328, AA278999, AA280712, AA281733, AA281871, AA282407, AA282626, AA283639, AA542810, AA557893, AA568486, AA569759, AA577522, AA659517, AA659737, AA664537, AA713950, AA805488, AA835999, AA876619, AA931568, AA935758, AA946722, AI000603, D82640
832539	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1508 of SEQ ID NO:400, b is an integer of 15 to 1522, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:400, and where b is greater than or equal to a + 14.	H72563, AA160114, AA159654, AA161261, AA165097, AA223618, AA243203
832554	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1356 of SEQ ID NO:401, b is an integer of 15 to 1370, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:401, and where b is greater than or equal to a + 14.	
832569	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1398 of SEQ ID NO:402, b is an integer of 15 to 1412, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:402, and where b is greater than or equal to a + 14.	
832578	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1736 of SEQ ID NO:403, b is an integer of 15 to 1750, where both a and b correspond to the positions of nucleotide	R09545, R09658, R09967, R11471, R16714, R16910, R16965, R19372, R80788, R80988, H28725, H63085, H63169, H75499, H75500, N33554, N41536, N52961, N52966, N74070, W01039, W57770, W57843, W60109,

	residues shown in SEQ ID NO:403, and where b is greater than or equal to a + 14.	W91978, W92107, AA001984, AA004653, AA027155, AA418427, AA281395, AA532870, AA564737, AA588889, AA631841, AA639548, AA765363, AA877896, AA887900, AA974026, AI057270, AI084214, AI094490, AI096750, AI097632, AI096745
832615	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1325 of SEQ ID NO:404, b is an integer of 15 to 1339, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:404, and where b is greater than or equal to a + 14.	
832620	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 468 of SEQ ID NO:405, b is an integer of 15 to 482, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:405, and where b is greater than or equal to a + 14.	
832632	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1399 of SEQ ID NO:406, b is an integer of 15 to 1413, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:406, and where b is greater than or equal to a + 14.	
832633	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1679 of SEQ ID NO:407, b is an integer of 15 to 1693, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:407, and where b is greater than or equal to a + 14.	R69173, AA053085, AA053597, AA427705, AA730380, AA865757, AA911497, AI083906
833483	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1328 of SEQ ID NO:408, b is an integer of 15 to 1342, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:408, and where b is greater than or equal to a + 14.	
834574	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 2403 of SEQ ID NO:409, b is an integer of 15 to 2417, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:409, and where b is greater than or equal to a + 14.	
834859	Preferably excluded from the present invention are	

	one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1387 of SEQ ID NO:410, b is an integer of 15 to 1401, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:410, and where b is greater than or equal to a + 14.	
834861	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 3002 of SEQ ID NO:411, b is an integer of 15 to 3016, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:411, and where b is greater than or equal to a + 14.	
834890	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 944 of SEQ ID NO:412, b is an integer of 15 to 958, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:412, and where b is greater than or equal to a + 14.	T40255, T40256, T40770, T40778, T40803, T41118, T94280, T94627, R13201, R32388, R32389, R53769, H28669, H39502, H42532, H42533, R82957, R85205, R85206, R88749, R90730, R90754, R91006, R92221, H56130, H56210, H58500, H57659, H69479, H69882, N22547, N31579, N42592, N45537, N48687, N56654, N58050, N69059, N73728, N80748, N92927, N94545, W20471, W30838, W52039, W60171, W68292, W93085, W93140, N91563, AA010850, AA011289, AA054592, AA054780, AA081135, AA081214, AA081655, AA081936, AA082127, AA082262, AA088665, AA088804, AA102560, AA100239, AA114237, AA115714, AA115715, AA127304, AA127303, AA147789, AA148021, AA149821, AA152050, AA160878, AA169126, AA171659, AA172131, AA172285, AA194597, AA243129, AA419357, AA425135, AA426203, AA244212, AA505963, AA508221, AA527434, AA527878, AA565036, F17736, AA582605, AA582728, AA583851, AA586421, AA601920, AA570580, AA574367, AA577515, AA577538, AA565998, AA657417, AA659655, AA662658, AA665113, AA714991, AA770684, AA808865, AA826971, AA838507, AA876809, AA877842, AA878025, AA886042, AA886643, AA877950, AA937751, AA948428, AA947036, AA973473, AA983150, AA989361, A1082367, D78922, D82096, N83321, C04115, R29685, C17110, C18023, C18068, AA093539, AA094947, AA151399, AA654145, AA654136
835079	Preferably excluded from the present invention are	N25566, W00985, AA081340,

	one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 486 of SEQ ID NO:413, b is an integer of 15 to 500, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:413, and where b is greater than or equal to a + 14.	AA152231, AA164282, AA171619, AA187113, AI073932
835554	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 3383 of SEQ ID NO:414, b is an integer of 15 to 3397, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:414, and where b is greater than or equal to a + 14.	
835560	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 2866 of SEQ ID NO:415, b is an integer of 15 to 2880, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:415, and where b is greater than or equal to a + 14.	
835723	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1602 of SEQ ID NO:416, b is an integer of 15 to 1616, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:416, and where b is greater than or equal to a + 14.	T71562, R11480, R19383, R25309, R46659, R48802, R48913, R50038, R50376, R54963, R46659, R70030, R70077, R70161, R71380, R72303, R72352, R72772, R72773, R73386, R73387, H15775, H15776, H25239, H27204, H30499, H42026, H42613, H43207, H43254, H44314, H44936, H44975, R98394, R98395, R99071, R99271, H58902, H58903, H73590, H73436, H75566, H80599, N40440, N48475, N59703, AA515035, AA515043, AA515450, AA515650, AA515746, AA551788, AA551943, AA554602, AA557281, AA581549, AA581554, AA587399, AA593890, AA593997, AA593998, AA568878, AA568962, AA622458, AA714206, AA728962, AA737738, AA738036, AA738486, AA847538, AA865069, AA872029, AA886612, AA903381, AA916458, AA916464, AA922563, AA928617, AA928314, AA934581, AA973769, AA973767, AA983480, AA991199, AA994932, AA995182, AA999704, AI028371, AA643041
835791	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1801 of SEQ ID NO:417, b is an integer of 15 to 1815, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:417, and where b is greater than or equal to a + 14.	

835817	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1952 of SEQ ID NO:418, b is an integer of 15 to 1966, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:418, and where b is greater than or equal to a + 14.	
835840	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 2838 of SEQ ID NO:419, b is an integer of 15 to 2852, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:419, and where b is greater than or equal to a + 14.	T66583, R15957, R22860, R62339, R62341, R62856, AA210836, AA214633, AA256340, AA732582, AA740735
836048	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 2691 of SEQ ID NO:420, b is an integer of 15 to 2705, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:420, and where b is greater than or equal to a + 14.	
836898	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1887 of SEQ ID NO:421, b is an integer of 15 to 1901, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:421, and where b is greater than or equal to a + 14.	
836927	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 2463 of SEQ ID NO:422, b is an integer of 15 to 2477, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:422, and where b is greater than or equal to a + 14.	
837344	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 763 of SEQ ID NO:423, b is an integer of 15 to 777, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:423, and where b is greater than or equal to a + 14.	
837789	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1635 of SEQ ID NO:424, b is an integer of 15 to 1649, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:424, and where b is greater than or equal to a + 14.	
838549	Preferably excluded from the present invention are	

	one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1594 of SEQ ID NO:425, b is an integer of 15 to 1608, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:425, and where b is greater than or equal to a + 14.	
838754	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1780 of SEQ ID NO:426, b is an integer of 15 to 1794, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:426, and where b is greater than or equal to a + 14.	
838768	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 756 of SEQ ID NO:427, b is an integer of 15 to 770, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:427, and where b is greater than or equal to a + 14.	
839486	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 498 of SEQ ID NO:428, b is an integer of 15 to 512, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:428, and where b is greater than or equal to a + 14.	
839561	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1456 of SEQ ID NO:429, b is an integer of 15 to 1470, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:429, and where b is greater than or equal to a + 14.	R61634, AA135004, AA159213
839816	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 420 of SEQ ID NO:430, b is an integer of 15 to 434, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:430, and where b is greater than or equal to a + 14.	
840068	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1809 of SEQ ID NO:431, b is an integer of 15 to 1823, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:431, and where b is greater than or equal to a + 14.	
840279	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide	

	sequence described by the general formula of a-b, where a is any integer between 1 to 3377 of SEQ ID NO:432, b is an integer of 15 to 3391, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:432, and where b is greater than or equal to a + 14.	
840489	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 2539 of SEQ ID NO:433, b is an integer of 15 to 2553, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:433, and where b is greater than or equal to a + 14.	
840538	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 2518 of SEQ ID NO:434, b is an integer of 15 to 2532, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:434, and where b is greater than or equal to a + 14.	T47551, T47552, T64522, T65947, R70190, H97064, N25641, N34240, N48063, N53261, N67904, N92702, N98774, W16899, W20316, W31028, W40137, W45371, W48722, W48577, W68670, W68773, W74242, AA033573, AA033574, AA063270, AA063271, AA065213, AA064894, AA082200, AA083707, AA085441, AA085694, AA088302, AA088303, AA099844, AA099984, AA102604, AA111894, AA112981, AA115039, AA115800, AA115799, AA122221, AA126905, AA126955, AA127109, AA127548, AA127549, AA128933, AA129152, AA129743, AA133290, AA135251, AA151963, AA156321, AA156382, AA160182, AA165104, AA164688, AA173757, AA180038, AA182644, AA190866, AA190959, AA191561, AA191637, AA197348, AA195895, AA258593, AA258622, AA262173, AA464978, AA465047, AA417938, AA418116, AA292727, AA523585, AA525020, AA548516, AA551816, AA554642, AA581720, AA568802, AA579801, AA738216, AA832441, AA903391, AA938688, AA977201, AA987552, AI095102, AI084149, W27768, C05889, C06263, AA089556, AA652586, AA213999, AA213977, AA219123, AA219290, AA435695, D12383, D12389, AA451677, AA453222, AA485641, AA485768, AA488670, AA485947, AA486053, AA486197, AA489511, AA489512, AA489558, AA491452, AA489876, AA600130, AA608644, AA620481, AA664307, AA629754, AA629909, AA677148, AA722910, AA772440, AA773550, AI038219, AI075755, AI081932, AI084706, T10852, T24678, F00208, F00897

840545	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1808 of SEQ ID NO:435, b is an integer of 15 to 1822, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:435, and where b is greater than or equal to a + 14.	
840549	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1016 of SEQ ID NO:436, b is an integer of 15 to 1030, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:436, and where b is greater than or equal to a + 14.	R10733, T86298, R55182, R55183, H00476, H00530, H25856, H25909, H25910, N50923, W84600, W84452, AA227897, D78774, AA486440, AA629249
840551	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1618 of SEQ ID NO:437, b is an integer of 15 to 1632, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:437, and where b is greater than or equal to a + 14.	
840557	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1002 of SEQ ID NO:438, b is an integer of 15 to 1016, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:438, and where b is greater than or equal to a + 14.	
840561	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 580 of SEQ ID NO:439, b is an integer of 15 to 594, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:439, and where b is greater than or equal to a + 14.	
840562	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1566 of SEQ ID NO:440, b is an integer of 15 to 1580, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:440, and where b is greater than or equal to a + 14.	R08937, R09046, R14796, R18307, R31150, R42283, R51828, R54224, R42283, R72104, R72156, R73118, R73171, R73943, H25904, H27191, H27192, H30471, H72478, H72879, H88214, H98231, W45061, W45071, W49842, W67423, W67424, W93880, W94151, AA023007, AA022473, AA032224, AA032282, AA034411, AA035691, AA040428, AA046861, AA046994, AA046313, AA046139, AA053780, AA101657, AA101658, AA167298, AA227543, AA227684, AA458877, AA459067, AA463656, AA464047, AA464754, AA225370, AA225425, AA225400, AA558796, AA582089, AA565830, AA713907,

		AA864510, AA936117, C01002, N86320, C04277, AA652714, AA402391, AA402565, AA479073, AA621791, AA670200, AA456544, AA676732, AA707089, AI014599, AI022852, AI023739, AI091873, AI094288, Z39517, Z43438
840564	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1068 of SEQ ID NO:441, b is an integer of 15 to 1082, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:441, and where b is greater than or equal to a + 14.	
840572	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1227 of SEQ ID NO:442, b is an integer of 15 to 1241, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:442, and where b is greater than or equal to a + 14.	T87514, T87515, H84879, AA001503, AA506411, AA508167, AA715396, AA931268, AA292666, AA478036, AA478193, AA478194, AA707886, AA724969, AA725050, AA779127, AA843885
840600	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 954 of SEQ ID NO:443, b is an integer of 15 to 968, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:443, and where b is greater than or equal to a + 14.	R38172, AA226748, AA484320, AA831852
840604	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1346 of SEQ ID NO:444, b is an integer of 15 to 1360, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:444, and where b is greater than or equal to a + 14.	
840608	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1821 of SEQ ID NO:445, b is an integer of 15 to 1835, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:445, and where b is greater than or equal to a + 14.	
840620	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1341 of SEQ ID NO:446, b is an integer of 15 to 1355, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:446, and where b is greater than or equal to a + 14.	R17303, R41982, R41982, H43756, N62762, AA053677, AA053697, AA084224, AA084019, AA084952, AA419123, AA419160, AA426014, AA425077, AA427847, AA524035, AA565019, AA632254, AA745726, AA835832, AA931712, AA932520, AA937139, AA961716, AA995607, AA453838, AA455030, AA476981, AA479615, AA482659, AA455837,

		AA488554, AA620470, AA781416, AA844227, AI090902, T19161
840625	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 361 of SEQ ID NO:447, b is an integer of 15 to 375, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:447, and where b is greater than or equal to a + 14.	
840626	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1379 of SEQ ID NO:448, b is an integer of 15 to 1393, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:448, and where b is greater than or equal to a + 14.	
840638	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1649 of SEQ ID NO:449, b is an integer of 15 to 1663, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:449, and where b is greater than or equal to a + 14.	H01158, H01159, H05751, H05858, H83341, H83695, N47512, N47513, W39756, W79733, W90027, W90155, AA047691, AA047741, AA086374, AA100549, AA159315, AA159414, AA282525, AA282633, AA595381, AA688093, AA744757, AA865203, AA933811, AA969838, AA975917, F18424, D12197, D12219, AA478596, AA665540, AA909221, AA969720, AI049820
840649	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1366 of SEQ ID NO:450, b is an integer of 15 to 1380, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:450, and where b is greater than or equal to a + 14.	R00133, R22651, R44356, R44356, R56353, R93194, N47106, N50316, N50780, N55139, AA010596, AA010597, AA012940, AA012888, AA013216, AA013313, AA017544, AA017417, AA047814, AA047792, AA235545, AA262268, AA262879, AA563873, AA570239, AA573586, AA827412, AA862337, AA902472, AA962409, AA971292, AA973596, AI056509, AI080455, AA410833, T23822, T16761
840651	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 912 of SEQ ID NO:451, b is an integer of 15 to 926, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:451, and where b is greater than or equal to a + 14.	
840666	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1628 of SEQ ID NO:452, b is an integer of 15 to 1642, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:452, and where b is greater than or equal to a + 14.	N32778, N34353, N34537, N41780, N42818, N93337, W25190, AA035229, AA035230, AA044070, AA044162, AA195074, AA195174, AA419441, AA731906, AA761315, AA761330, AA766382, AA766593, AA769537, AA805515, AA806516, AA809893, AA814954, AA857917, N44554,

		AA393941, AI074651, T10618, Z35722
840681	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 2240 of SEQ ID NO:453, b is an integer of 15 to 2254, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:453, and where b is greater than or equal to a + 14.	
840682	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1917 of SEQ ID NO:454, b is an integer of 15 to 1931, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:454, and where b is greater than or equal to a + 14.	
840684	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 757 of SEQ ID NO:455, b is an integer of 15 to 771, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:455, and where b is greater than or equal to a + 14.	
840697	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1155 of SEQ ID NO:456, b is an integer of 15 to 1169, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:456, and where b is greater than or equal to a + 14.	R00751, R02584, R02703, R69879, R69927, H13156, H29249, H29248, H41216, R83398, H54666, H54667, H73551, H73552, H90468, H91760, H97869, N31729, N31735, N51232, W32147, W32175, W44313, W45660, W57760, W57761, W68386, W68502, W68752, W68835, W72538, W76163, AA035740, AA043246, AA043585, AA044419, AA043053, AA047593, AA047601, AA088798, AA147253, AA155747, AA160105, AA165689, AA172386, AA173747, AA189005, AA189006, AA471066, AA507210, AA513086, AA516406, AA514685, AA635861, AA657400, AA668796, AA737126, AA768005, AA768358, AA887459, AA977176, D80509, D81008, D81471, D81800, D82666, N83795, AA643662, AA284937, AA290823, AA447984, AA448126, AA676807, AA709464, AA780333, AA843801, AA853391, AA868403, AA917460, T17166, T17177, T16671, T48481, T48507
840698	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 3235 of SEQ ID NO:457, b is an integer of 15 to 3249, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:457, and where b is	

	greater than or equal to a + 14.	
840708	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1902 of SEQ ID NO:458, b is an integer of 15 to 1916, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:458, and where b is greater than or equal to a + 14.	R21272, R45362, R45362, H06049, H13385, AA082768, AA101114, AA131634, AA131718, AA152290, AA150232, AA418083, AA418230, AA422115, AA424919, AA426139, AA741277, AA749290, AA811505, AA836102, AA411231, AA453804, AA453890, AA758905, AA769817, AA770192, AA904708, AA905158, AA969156, AI093952, Z42470, Z41665, Z44053
840714	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 2759 of SEQ ID NO:459, b is an integer of 15 to 2773, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:459, and where b is greater than or equal to a + 14.	
840716	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 2017 of SEQ ID NO:460, b is an integer of 15 to 2031, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:460, and where b is greater than or equal to a + 14.	
840721	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1825 of SEQ ID NO:461, b is an integer of 15 to 1839, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:461, and where b is greater than or equal to a + 14.	
840735	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 765 of SEQ ID NO:462, b is an integer of 15 to 779, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:462, and where b is greater than or equal to a + 14.	T47277, T56085, T93319, T85388, H57620, H58465, N77902, N80219, N93978, W19715, W37380, W37643, W38508, W38722, W47048, W68079, W67976, W69349, W69350, AA025313, AA024560, AA063371, AA063370, AA463222, AA463223, AA424422, AA469264, AA480510, AA507733, AA524348, AA557233, AA602394, AA603318, AA631014, AA569554, AA575944, AA688112, AA911131, AA932225, AA937015, AA994856, AI077707, N92552, W00604, C00184, AA292823, AA401683, AA663906, AA664122, AA771943, AA779608, AA812529, AI028120, AI027559, AI032511, AI033880, AI034204, AI078458, AI041685, D31473, T64469
840738	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide	

	sequence described by the general formula of a-b, where a is any integer between 1 to 1703 of SEQ ID NO:463, b is an integer of 15 to 1717, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:463, and where b is greater than or equal to a + 14.	
840745	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 814 of SEQ ID NO:464, b is an integer of 15 to 828, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:464, and where b is greater than or equal to a + 14.	
840747	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1159 of SEQ ID NO:465, b is an integer of 15 to 1173, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:465, and where b is greater than or equal to a + 14.	
840756	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 507 of SEQ ID NO:466, b is an integer of 15 to 521, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:466, and where b is greater than or equal to a + 14.	AA074254
840776	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1414 of SEQ ID NO:467, b is an integer of 15 to 1428, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:467, and where b is greater than or equal to a + 14.	T47069, T47068, T63511, T63587, T79637, T79722, R36141, R36419, R65831, R65934, R69612, R69701, H00464, H00514, H04572, H04575, H12602, H12652, H13166, H66218, H67195, H67868, H67868, N62959, W92249, W92250, W92609, W95234, AA007598, AA193373, AA195360, AA195359, AA425046, AA430627, AA428172, AA484871, AA557201, AA902998, AA927360, N79862, AA479674, AA477192, AA481418, AA481651, AA495983, AA496377, AA496655, AA912146, AA912181, AI049805, AA693485
840784	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 3449 of SEQ ID NO:468, b is an integer of 15 to 3463, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:468, and where b is greater than or equal to a + 14.	
840788	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 607 of SEQ ID	

	NO:469, b is an integer of 15 to 621, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:469, and where b is greater than or equal to a + 14.	
840794	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1819 of SEQ ID NO:470, b is an integer of 15 to 1833, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:470, and where b is greater than or equal to a + 14.	
840797	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 3188 of SEQ ID NO:471, b is an integer of 15 to 3202, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:471, and where b is greater than or equal to a + 14.	
840799	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 927 of SEQ ID NO:472, b is an integer of 15 to 941, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:472, and where b is greater than or equal to a + 14.	
840818	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1265 of SEQ ID NO:473, b is an integer of 15 to 1279, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:473, and where b is greater than or equal to a + 14.	
840822	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 3195 of SEQ ID NO:474, b is an integer of 15 to 3209, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:474, and where b is greater than or equal to a + 14.	T47621, T77305, T83423, R18484, R51973, R51974, R73192, H06082, H12940, H27135, H45895, H45904, N72089, W00342, W52213, W96404, AA045488, AA058907, AA062768, AA069032, AA081439, AA082427, AA084417, AA101216, AA234022, AA534011, AA565390, AA588319, AA588430, AA568701, AA635907, AA579930, AA827039, AA857519, AA872490, AA904077, AA995057, AI073336, N95359, C15883, AA781445, AA906492, AI037943, AI039428
840830	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 819 of SEQ ID NO:475, b is an integer of 15 to 833, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:475, and where b is	N33920, N33932, N49642, N49629, AA508747, AA514767, AA583465, AA805203, AA878968, U37231, T24573

	greater than or equal to a + 14.	
840846	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1127 of SEQ ID NO:476, b is an integer of 15 to 1141, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:476, and where b is greater than or equal to a + 14.	T68706, T68719, T68771, T68784, T73424, T73431, T73486, T73492, T73499, T73535, T89865, R11465, T79345, T79774, T81799, T82119, T82855, T96198, T96454, T96686, T96802, T96920, T97027, T99996, T99997, R00156, R00157, R83404, R85816, R91357, R93314, R94713, R94794, R97348, R99024, R99798, H48280, H48369, H48754, H54738, H54739, H55985, H55984, H56050, H56244, H57662, H57872, H57873, H58502, H60170, H60211, H62933, H69203, H69228, H69229, H71630, H73011, H73012, H81193, H81194, H90826, H91385, N33963, N49672, N49822, N52577, N54836, N58435, N64440, N66934, N69249, N69373, N74062, N75759, N78025, N78145, N94249, N95116, W03303, W01169, W01912, N91401, AA025243, AA026028, AA193126, AA194255, AA236507, AA242995, AA622239, AA575858, AA575872, AA576026, AA576150, AA576597, AA864932, AA877934, AA969761, AA994970, AI017867, D82634, C21067, AA431221, AA779655, AA782374, AA812640, AA923315, AA962377, AA993251, AI018445, AI025584, AI092470, T79311
840848	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1088 of SEQ ID NO:477, b is an integer of 15 to 1102, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:477, and where b is greater than or equal to a + 14.	R10066, R10163, T26606, R61067, R72646, H08322, H47858, H47859, R86048, H68866, H68867, H69098, H82364, N58491, N78080, W52876, W60083, AA043086, AA045865, AA045866, AA055712, AA057298, AA058743, AA079887, AA079888, AA099233, AA099234, AA102153, AA113213, AA115932, AA121000, AA131067, AA143412, AA146598, AA155632, AA155688, AA160447, AA173257, AA173248, AA195987, AA196375, AA233537, AA463552, AA503072, AA551794, AA586410, AA594814, AA613123, AA573356, AA580449, AA731195, AA742856, AA827930, AA863440, AA865529, AA876847, AA953614, AA976924, N84278, N88762, C17112, AA219765, AA284503, AA293437, AA293046, AA669435, AA722103, AI027785, AI073617, AI092707, T17392, F08770, D12026
840860	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide	T89645, T89919, T93704, R21871, R22387, R78094, R78181, R78515,

	sequence described by the general formula of a-b, where a is any integer between 1 to 4187 of SEQ ID NO:478, b is an integer of 15 to 4201, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:478, and where b is greater than or equal to a + 14.	R78560, H40124, H41731, N28359, N42893, N62851, N64787, N67463, N76199, N77065, N77758, W67341, W68381, AA034244, AA044935, AA045056, AA057392, AA057684, AA071214, AA071442, AA081937, AA082360, AA082229, AA082230, AA082708, AA083297, AA083188, AA127585, AA149575, AA151791, AA167113, AA173360, AA191227, AA195437, AA223329, AA223614, AA243268, AA261939, AA262815, AA262816, AA422160, AA426276, AA225924, AA504466, AA504634, AA522823, AA554566, AA632813, AA576873, AA662886, AA730326, AA748669, AA828942, AA837197, AA857065, AA857683, AA862276, AA864246, AA873317, AI083733, D82604, D82635, N81179, N85023, N85166, N85712, C00193, C00199, C02425, N87331, N88683, N88852, N89408, C02916, C05151, C06382, AA642209, C21319, AA091285, AA091688, AA094300, AA205974, AA206268, AA206598, AA205324, AA649340, AA247212, AA404505, AA421263, AA421361, D11545, AA441853, AA441826, AA463350, AA463858, AA487271, AA487388, AA496439, AA496488, AA634627, AA663685, AA665466, AA456144, AA722996, AA772136, AA772153, AA774179, AA992418, AI076734, T10506, Z30218, Z38961, T16262, T48571, D31110, D45597, F06042, F00682
840861	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 773 of SEQ ID NO:479, b is an integer of 15 to 787, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:479, and where b is greater than or equal to a + 14.	T52180, T52256, T57048, T60934, T60993, T94137, T94228, T91060, T85924, R23216, R23292, R31316, R31576, R62640, R62693, H03198, H18231, H18269, H22414, H26112, H26116, H26378, H40754, H38895, H47721, H48072, R89134, R89141, R91829, R91836, R98452, H65626, H65627, H69728, H71913, H71914, H78844, H80090, H83062, H84585, H87467, H87577, H93457, H93458, N23179, N30549, N32644, N39052, N40455, N48060, N48244, N53258, N53755, N63557, N94559, N94883, N94981, N95791, N42987, W19445, W19573, W23831, W24902, W30850, W32700, W32701, W37523, W56867, W60497, W60972, W61219, W69268, W69346, W80426, W80556, W94817, W95832, W95966, W96035, W96092,

		N90310, AA010147, AA010148, AA025440, AA025757, AA027347, AA027822, AA027874, AA029650, AA029651, AA037779, AA039260, AA046801, AA046818, AA054707, AA058654, AA062684, AA063287, AA074876, AA074979, AA084381, AA085264, AA085328, AA085598, AA122190, AA120978, AA133892, AA129630, AA172403, AA172206, AA190489, AA190525, AA464455, AA464996, AA225769, AA259210, AA483109, AA483741, AA493542, AA502162, AA516183, AA522567, AA526813, AA557654, AA588882, AA593799, AA576216, AA659530, AA662308, AA688246, AA688254, AA687457, AA687516, AA689236, AA728852, AA729032, AA747479, AA747979, AA831447, AA887348, AA903105, AA916516, AA934714, AA953363, AA976759, AA991410, AA991434, AI002147, AI028033, N83338, C02469, R29174, AA090669, AA092066, AA648634, AA443968, AA444149, AA482243, AA482340, AA485406, AA598458, AA644566, AA664032, AA680199, AA676482, AA629708, AA630110, AA457100, AA431269, AA405296, AA405332, AA721997, AA724146, AA774657, AA781529, AA781641, AA781838, AA782849, AA813171, AA843229, AA846744, AA846814, AA854299, AA854765, AA789029, AA993047, AI023973, AI027725, AI031943, AI038463, AI041602, AI085085, AI086504, AI088189
840871	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 717 of SEQ ID NO:480, b is an integer of 15 to 731, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:480, and where b is greater than or equal to a + 14.	H42821, AA028094, AA099211, AA160368, AA223572, AA232552, AA252811
840874	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1105 of SEQ ID NO:481, b is an integer of 15 to 1119, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:481, and where b is greater than or equal to a + 14.	
840878	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b,	T40405, T41252, T47240, T47241, T50233, T52891, T57110, T58359, R19508, R43858, R43858, R75598,

	where a is any integer between 1 to 2042 of SEQ ID NO:482, b is an integer of 15 to 2056, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:482, and where b is greater than or equal to a + 14.	R75665, H13192, H13193, N25264, N31900, N42683, N72995, N93388, W25360, W47628, W47629, AA009691, AA009410, AA045777, AA045910, AA063040, AA063076, AA130044, AA149205, AA149206, AA191678, AA252698, AA464304, AA225264, AA514845, AA526726, AA548411, AA548704, AA552050, AA552558, AA568675, AA827017, AA834447, AA838450, AA886357, AA886653, AA887879, AA916602, AA928685, AA968793, AI005016, W28859, AA134038, AA455118, AA496380, AA496656, AA598830, AA653270, AA725217, AA733068, AI004394, AI023815, AI026954, AI040891, Z25388, Z28470, AA702322
840880	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 873 of SEQ ID NO:483, b is an integer of 15 to 887, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:483, and where b is greater than or equal to a + 14.	H02306, H02418, N48196, N53344, AA059013, AA506159, AA613938, AA662759, AA976725, AA854631
840884	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1864 of SEQ ID NO:484, b is an integer of 15 to 1878, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:484, and where b is greater than or equal to a + 14.	
840907	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1552 of SEQ ID NO:485, b is an integer of 15 to 1566, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:485, and where b is greater than or equal to a + 14.	
840926	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 3032 of SEQ ID NO:486, b is an integer of 15 to 3046, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:486, and where b is greater than or equal to a + 14.	
840932	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1890 of SEQ ID NO:487, b is an integer of 15 to 1904, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:487, and where b is	

	greater than or equal to a + 14.	
840940	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 813 of SEQ ID NO:488, b is an integer of 15 to 827, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:488, and where b is greater than or equal to a + 14.	
840947	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1912 of SEQ ID NO:489, b is an integer of 15 to 1926, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:489, and where b is greater than or equal to a + 14.	
840959	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1447 of SEQ ID NO:490, b is an integer of 15 to 1461, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:490, and where b is greater than or equal to a + 14.	
840964	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 791 of SEQ ID NO:491, b is an integer of 15 to 805, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:491, and where b is greater than or equal to a + 14.	R79226, H12332, H51062, H83364, H89523, N27508, N30527, N40233, N52503, N53855, N94367, AA055215, AA055306, AA188169, AA468498, AA470473, AA563662, AA622643, AA579613, AA668790, AA748160, AA765447, AA873430, AA879079, AA903275, AA970424, N73354, AA402259, AA883758, AA890505, AA906005, AI023931
840979	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 2255 of SEQ ID NO:492, b is an integer of 15 to 2269, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:492, and where b is greater than or equal to a + 14.	
840984	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 4094 of SEQ ID NO:493, b is an integer of 15 to 4108, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:493, and where b is greater than or equal to a + 14.	
840986	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 2195 of SEQ ID NO:494, b is an integer of 15 to 2209, where both a and b correspond to the positions of nucleotide	H25393, H25394, H25511, H25512, R95750, R95794, H64076, H64131, H68715, H80548, H80604, H94681, H95039, H99481, N28293, N30167, N35782, W47389, W47262, W61304, W65368, AA054346, AA054383,

	residues shown in SEQ ID NO:494, and where b is greater than or equal to a + 14.	AA058320, AA058448, AA512954, AA558416, AA588459, AA935690, AI097565, N87339, AA993027, AA993568, AA701454, AA702350
840988	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1663 of SEQ ID NO:495, b is an integer of 15 to 1677, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:495, and where b is greater than or equal to a + 14.	T87048, R24473, R43337, R43337, N75007, W05750, AA182467, AA227466, AA504464, AA504538, AA923479, AA648887, AA663889, AI027636, AI028506, AI026720, Z42717
840990	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1688 of SEQ ID NO:496, b is an integer of 15 to 1702, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:496, and where b is greater than or equal to a + 14.	
840992	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 2362 of SEQ ID NO:497, b is an integer of 15 to 2376, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:497, and where b is greater than or equal to a + 14.	
841009	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 826 of SEQ ID NO:498, b is an integer of 15 to 840, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:498, and where b is greater than or equal to a + 14.	T40334, T41195, T79150, T79231, T85615, T98895, T99485, R25796, H03311, H03312, H11314, H21245, R91754, R91755, R93025, R97834, R97886, R99577, R99583, R99683, R99689, H88057, H97799, H97870, N34019, N35363, N42786, N44738, N52502, N70158, N72884, N74746, N93542, N95357, N98354, W01181, W03108, W15165, W19587, W21350, W24700, W24805, W39226, W48682, W49637, W49739, W51977, W67546, W67528, W67665, W79731, W93828, W93829, AA025348, AA025356, AA024401, AA024402, AA029589, AA029588, AA099331, AA099865, AA121627, AA126717, AA126816, AA126817, AA133155, AA165162, AA165163, AA557332, AA640015, AA579505, AA665011, AA665221, AA738009, AA830748, AA918150, AA918992, AA947223, AA974955, AI083731, N56157, N89240, AA092060, AA094384, AA650291, AA292814, AA402491, F20671, F21115, D11655, D11564, D11605, D12048, AA634049, U54738, AA732766, AA782030, AA843638, AA860477, AA861482, AI018649,

		AI092171, Z28714, T23956, AA694568
841012	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 447 of SEQ ID NO:499, b is an integer of 15 to 461, where both a and b correspond to the positions of nucleotide . residues shown in SEQ ID NO:499, and where b is greater than or equal to a + 14.	
841016	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 2768 of SEQ ID NO:500, b is an integer of 15 to 2782, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:500, and where b is greater than or equal to a + 14.	R21854, R21868, R23349, R27518, R63726, R63775, R65731, R65957, R65958, R66192, R66977, R66978, R67072, R69600, R69690, H12415, H12416, N46541, N47260, N47778, N48572, N51984, N95008, W25613, W31713, W32142, W38029, W38650, W38655, AA034256, AA037658, AA037660, AA039268, AA042908, AA042921, AA063533, AA126558, AA130121, AA130157, AA137270, AA136020, AA232954, AA233044, AA429346, AA429872, AA565520, AA604780, AA610435, AA631349, AA631518, AA740206, AA770618, AA912228, AI079705, N84191, N85956, N92894, W38030, C00380, N83173, C03262, AA092010, U82782, AA247592, AA284977, AA283619, AA291890, AA293636, AA410312, AA410537, AA453566, AA487623, AA626442, AA628932, AA629190, AA629753, AA629916, AA719528, AA843073, AA844228, AA890492, AI024670, AI051881, AI061324, T11149
841017	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1235 of SEQ ID NO:501, b is an integer of 15 to 1249, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:501, and where b is greater than or equal to a + 14.	R21764, R21815, N71125, W17312, AA112660, AA179538, AA179507, AA902202, AA907419, AA913594, AA994481, AI049652
841021	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1344 of SEQ ID NO:502, b is an integer of 15 to 1358, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:502, and where b is greater than or equal to a + 14.	R23836, W38704, AA033686, AA176734, AA192268, AA525913, AA531505, AA532666, AA533781, AA533827, AA533949, AA554396, AA576754, AA906883, N24273, C14272, C14285, C14286, C18998
841032	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 487 of SEQ ID NO:503, b is an integer of 15 to 501, where both a and b correspond to the positions of nucleotide	T41136, T52990, T52991, T61494, T63001, T63145, T87321, T87328, T89480, T84361, R05264, N75935, W05120, W25352, AA191627, AA258512, AA418549, AA224774, AA225253, AA229538, AA229537,

	residues shown in SEQ ID NO:503, and where b is greater than or equal to a + 14.	AA229951, AA230318, AA468106, AA468170, AA482814, AA482855, AA482894, AA482906, AA483676, AA491563, AA491627, AA492175, AA501375, AA502205, AA505498, AA508058, AA508125, AA512979, AA513165, AA523347, AA528170, AA531497, AA542840, AA551430, AA553992, AA554420, AA582164, AA583205, AA593192, AA593362, AA602125, AA603378, AA603728, AA617691, AA622865, AA630937, AA631991, AA570802, AA569520, AA654990, AA664728, AA664864, AA665278, AA729616, AA729639, AA729652, AA730512, AA730705, AA730910, AA737300, AA737303, AA736808, AA736909, AA738098, AA740165, AA740553, AA742574, AA742885, AA746988, AA747057, AA747094, AA747099, AA747961, AA748108, AA804727, AA805835, AA834105, AA838466, AA864527, AA872303, AA875939, AA876612, AA876936, AA879219, AA885735, AA886033, AA888159, AA888528, AA888683, AA903652, AA935001, AA948734, AA947836, AA978250, AA994661, AI073926, AI085517, N83676, N86451, N87989, AA642538, AA090432, AA090481, AA092225, AA091643, AA094678, AA094818, AA095214, AA648652, AA649783, AA650377, AA401641, F21163, AA411822, AA442212, AA609798, AA679909, F22052, AA679265, AA722456, AI003421, AI028430, AI077884, AI086743, T89286, R05321, AA694044
841051	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1997 of SEQ ID NO:504, b is an integer of 15 to 2011, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:504, and where b is greater than or equal to a + 14.	AA427363
841064	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1975 of SEQ ID NO:505, b is an integer of 15 to 1989, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:505, and where b is greater than or equal to a + 14.	R95695, H49073, H61707, H61911, H68517, H89719, H89781, H89828, H90680, N76870, W88654, W88898, AA046748, AA053076, AA053592, AA127256, AA127257, AA187351, AA188218, H67307, AA602545, AA720701, AA742288, N87596, AA094084, AA204976, AA676787, AA703221, AA779414, AI038609, AI074626, AI088527, T17364,

		AA702787
841069	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1071 of SEQ ID NO:506, b is an integer of 15 to 1085, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:506, and where b is greater than or equal to a + 14.	
841072	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1471 of SEQ ID NO:507, b is an integer of 15 to 1485, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:507, and where b is greater than or equal to a + 14.	
841078	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1916 of SEQ ID NO:508, b is an integer of 15 to 1930, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:508, and where b is greater than or equal to a + 14.	T39937, T68962, T84426, R20697, R36425, R45643, R45643, R68137, R70943, R70957, R70996, R71011, H02222, H05658, H05659, H25177, H29362, H54732, H54733, H60311, H60310, H77561, H77562, H78245, H78446, H82436, H82699, N20477, N57742, N59418, N59709, N76617, AA029237, AA055009, AA055434, AA236337, AA425703, AA427773, AA482193, AA482287, AA612777, AA729757, AA737276, AA744359, AA872776, AA972581, C06045, AA446583, AA449748, AA707197, AA757691, AA774691, AA992571, AI003756, AI027513, AI039704, AI042272, AI052652, AI077380, AI083949, AA774036
841080	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1120 of SEQ ID NO:509, b is an integer of 15 to 1134, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:509, and where b is greater than or equal to a + 14.	
841088	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1368 of SEQ ID NO:510, b is an integer of 15 to 1382, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:510, and where b is greater than or equal to a + 14.	R00895, R21561, R42090, R42090, H05080, N79589, N94381, W16578, W42724, W42813, W46346, W46347, W47346, W57707, W57783, AA070469, AA490938, AA586820, AA580196, AA745683, AA809239, AA931405, D11601, AA725448, AA992145, AI023735, AI025359, AI031575, AI033697, AI038145, AI093535, F00072
841092	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1727 of SEQ ID	

	NO:511, b is an integer of 15 to 1741, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:511, and where b is greater than or equal to a + 14.	
841095	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1516 of SEQ ID NO:512, b is an integer of 15 to 1530, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:512, and where b is greater than or equal to a + 14.	W20114, AA255840, AA568302, AA406006, AA434170
841096	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 2985 of SEQ ID NO:513, b is an integer of 15 to 2999, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:513, and where b is greater than or equal to a + 14.	
841102	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 2034 of SEQ ID NO:514, b is an integer of 15 to 2048, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:514, and where b is greater than or equal to a + 14.	
841104	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 3286 of SEQ ID NO:515, b is an integer of 15 to 3300, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:515, and where b is greater than or equal to a + 14.	T93851, R05295, R05354, R71097, R71445, R99396, N53129, W38359, W38417, W38418, W39384, W44785, W44786, W69719, W69847, W73703, AA134718, AA164646, AA164647, AA418958, AA420439, AA420440, AA548241, AA548224, AA558195, W73847, Z19840, AA707354, AA868898, AA917430, AI073454, F09131, F11469, AA700476
841108	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 3411 of SEQ ID NO:516, b is an integer of 15 to 3425, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:516, and where b is greater than or equal to a + 14.	T89709, T89806, T91163, T93774, T93819, T95226, R06420, R06475, R23277, R23370, R32742, R32743, R52354, R52355, R64095, R64184, R65984, R65985, R70225, R70226, R76344, R76672, R80205, H00679, H00770, H04254, H24758, H24803, H40273, H38053, H38054, H47116, H47210, R92478, R94873, R94872, H57866, H57867, H59353, H61105, H63261, H63535, H63938, H67759, H67760, H77384, H77385, H82932, H87435, H87541, H88753, H88754, N59081, N59489, N63682, N63939, N66851, N70709, N92122, N99845, W32595, W88585, W90769, W90327, W93082, W93137, AA025425, AA041232, AA114914, AA114913, AA128525, AA235362, AA235944,

		AA235945, AA425197, AA636023, AA639557, AA729723, AA907495, AI056355, AI089809, AA448599, AA449742, AA476262, AA478567, AA478700, AA599706, AA634117, AA677126, AA716562, AA923333, AA948589, AI051569, AI073816, AI074666, AI080341, AI084428, AI090962, AI096407
841118	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1344 of SEQ ID NO:517, b is an integer of 15 to 1358, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:517, and where b is greater than or equal to a + 14.	R20815, R36529, R38448, R46586, R46586, R71122, R71625, R77658, R80438, R80643, H12595, H12644, H99733, N20132, N25939, N29738, N57157, N59874, N67154, N67834, W03438, W04625, W31524, AA044199, AA044996, AA135739, AA135782, AA146912, AA146911, AA173589, AA224431, AA232224, AA256600, AA256599, AA419270, AA419321, AA425195, AA484744, AA507823, AA513832, AA584296, AA600955, AA614813, AA807248, AA904059, AA937796, AA973678, AA983325, AA991604, W01284, C16969, AA476260, AA476318, AA476367, AA609550, AA678511, AA722726, AA904676, AA954468, AI001869, AI031538, Z41297
841119	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1354 of SEQ ID NO:518, b is an integer of 15 to 1368, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:518, and where b is greater than or equal to a + 14.	R18472, W39766, AA076303, AA985235
841124	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 919 of SEQ ID NO:519, b is an integer of 15 to 933, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:519, and where b is greater than or equal to a + 14.	
841137	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1416 of SEQ ID NO:520, b is an integer of 15 to 1430, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:520, and where b is greater than or equal to a + 14.	T65560, R52978, R59392, H24368, H25185, N33308, AA016160, AA019434, AA082036, AA099724, AA099725, AA101466, AA100553, AA100634, AA100635, AA143046, AA150250, AA151129, AA165491, AA172129, AA176104, AA176248, AA176272, AA197310, AA227454, AA232220, AA243156, AA261904, AA262541, AA458854, AA459044, AA481155, AA493247, AA514323, AA522820, AA558368, AA582973, AA604489, AA640528, AA569125,

		AA569824, AA737640, AA743846, AA808232, AA812222, AA847813, AA865060, AA872242, AA872353, AA922866, AA933823, AA988358, AI056397, AI085865, AI088865, AA205921, AA205923, AA205997, AA204887, AA205731, D11887, AA634040, AA703823, AA703893, Z20424, AA707344, AA707416, AA716243, AA683201, AA890456, AI003274, AI076618, AI090177, T10877, Z28746, T25145, Z40353, F11026, F09670, AA699695, AA701137
841143	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1155 of SEQ ID NO:521, b is an integer of 15 to 1169, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:521, and where b is greater than or equal to a + 14.	T52948, T57468, T59332, T91403, T84637, R69314, R69315, R77481, R77675, R77676, H30692, H70576, N24036, N24905, N26173, N35858, N36029, W39771, W45303, W80648, W80649, AA029895, AA029983, AA036639, AA036850, AA043430, AA043431, AA046109, AA046196, AA076106, AA076107, AA083131, AA083181, AA083285, AA083293, AA147761, AA147804, AA155831, AA155741, AA430082, AA581553, AA593886, AA594233, AA604399, AA576339, AA715836, AA730946, AA737298, AA768251, AA872423, AA888276, AA961744, AA962699, AA975874, AI000132, R29417, AA640954, AA094702, AA398483, AA402600, AA489817, AA489948, AA496290, AA663953, AA663986, AA725581, AA771972, AA781165, AA845829, AA772618, AA773208, AA907551, AI003883, AI004593, AI031669, AI052123, AI085380
841148	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 2148 of SEQ ID NO:522, b is an integer of 15 to 2162, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:522, and where b is greater than or equal to a + 14.	
841149	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 785 of SEQ ID NO:523, b is an integer of 15 to 799, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:523, and where b is greater than or equal to a + 14.	AA812937
841151	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b,	

	where a is any integer between 1 to 1708 of SEQ ID NO:524, b is an integer of 15 to 1722, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:524, and where b is greater than or equal to a + 14.	
841155	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 548 of SEQ ID NO:525, b is an integer of 15 to 562, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:525, and where b is greater than or equal to a + 14.	
841161	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 2009 of SEQ ID NO:526, b is an integer of 15 to 2023, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:526, and where b is greater than or equal to a + 14.	H81836, AA015599, AA099033, AA099034, AA211818, AA741499, AA748367, AA768854, AA805297, AA804217, AI000120, AI090415, D79280, D79875, AA628397, AA628438, AA889584, Z36757
841162	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 2833 of SEQ ID NO:527, b is an integer of 15 to 2847, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:527, and where b is greater than or equal to a + 14.	T54529, T54568, T39916, T40885, T64421, T64740, T94433, T94519, T94763, T94764, T67443, T67536, T69533, R08782, R08783, T84049, T86084, R18023, R19657, R33054, R33948, R52119, R52216, R53248, R53249, R71311, H04393, H04418, H23196, H23309, H47118, R95161, H54791, H54843, H66487, H66488, H87522, H87523, H92220, H97204, H97637, H98041, N25008, N27036, N32850, N32940, N41677, N41803, N52911, N55243, N55603, N59425, N62367, N67146, N67527, N68040, N68109, N69439, N79136, W03264, W02511, W16533, W16511, W16949, W19590, W20032, W25683, W56022, W57870, W58141, W84752, W84757, W96458, W96558, N89892, N91494, AA035714, AA040577, AA040675, AA043889, AA052991, AA053277, AA053702, AA062923, AA063530, AA074314, AA074909, AA074744, AA076274, AA098982, AA099025, AA146894, AA146893, AA160127, AA160126, AA160195, AA160196, AA169764, AA169385, AA179301, AA223348, AA233558, AA235471, AA460676, AA420533, AA506563, AA523418, AA527621, AA528362, AA531060, AA532619, AA541282, AA552184, AA564466, AA564790, H98795, AA583450, AA613483, AA622733, AA627809, AA577550, AA578980, AA579413, AA714153, AA721494, AA721786, AA737104,

		AA738062, AA745852, AA746662, AA748113, AA814512, AA814515, AA848156, AA858182, AA877787, AA886219, AA886814, AA908510, AA919073, AA953828, AA971838, AA974669, AA974937, AA975070, AA978156, AA985412, AA985429, AA989103, AA989168, AA975750, AI053418, AI053736, AI053892, AI053967, AI053988, AI054073, AI054111, F18748, AI096767, W16689, F17979, W26593, W74635, R29761, AA090571, AA090284, AA092279, AA092676, AA174176, AA206002, AA206857, AA206939, AA204847, AA204862, AA205665, AA205777, C17805, AA215924. AA284942, AA285094, AA292514, AA293872, AA398296, AA401676, AA412021, AA450108, AA450173, AA477960, AA478675, AA479216, AA482218, AA608548, AA634838, AA634910, AA634951, AA644321, AA664196, AA665979, AA668238, AA668579, AA669764, AA669856, AA676279, AA630300, Z20366, AA716371, AA716380, Z19906, AA777040, AA778451, AA781061, AA845834, T25435, Z21568, AA772588, AA917780, AI003327, AI016140, AI024969, AI032559, AI056850, AI088269, AI090536, AI092597, AI093387, T15364, D29035, T27400, T27473, F02321, F06069, T69476, AA773898, AA694154
841163	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 802 of SEQ ID NO:528, b is an integer of 15 to 816, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:528, and where b is greater than or equal to a + 14.	T70512, W58177, W58266, AA027003, AA047260, AA057146, AA076110, AA150122, AA150030, AA424246, AA425670, AA523788, AA554661, AA582491, AA587000, AA633476, AA578397, AA662364, AA687611, AA729856, AA741041, AA806947, AA894899, AA922687, AA934486, AA946779, AA954606, AA962108, AA988276, AI054171, AA436000, AA436099, AA442324, AA451996, AA722958, AA780203, T25797, AI018410, AI024726, AI074321
841169	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 871 of SEQ ID NO:529, b is an integer of 15 to 885, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:529, and where b is greater than or equal to a + 14.	
841172	Preferably excluded from the present invention are	T47968, H14181, H26893, N40884,

	one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 728 of SEQ ID NO:530, b is an integer of 15 to 742, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:530, and where b is greater than or equal to a + 14.	Z42735
841174	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 511 of SEQ ID NO:531, b is an integer of 15 to 525, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:531, and where b is greater than or equal to a + 14.	
841179	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1911 of SEQ ID NO:532, b is an integer of 15 to 1925, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:532, and where b is greater than or equal to a + 14.	
841183	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 488 of SEQ ID NO:533, b is an integer of 15 to 502, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:533, and where b is greater than or equal to a + 14.	
841186	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1786 of SEQ ID NO:534, b is an integer of 15 to 1800, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:534, and where b is greater than or equal to a + 14.	
841204	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 2483 of SEQ ID NO:535, b is an integer of 15 to 2497, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:535, and where b is greater than or equal to a + 14.	
841206	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 4076 of SEQ ID NO:536, b is an integer of 15 to 4090, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:536, and where b is greater than or equal to a + 14.	
841207	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide	AA215286

	sequence described by the general formula of a-b, where a is any integer between 1 to 572 of SEQ ID NO:537, b is an integer of 15 to 586, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:537, and where b is greater than or equal to a + 14.	
841211	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1236 of SEQ ID NO:538, b is an integer of 15 to 1250, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:538, and where b is greater than or equal to a + 14.	
841225	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1336 of SEQ ID NO:539, b is an integer of 15 to 1350, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:539, and where b is greater than or equal to a + 14.	
841229	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 2495 of SEQ ID NO:540, b is an integer of 15 to 2509, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:540, and where b is greater than or equal to a + 14.	
841237	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1729 of SEQ ID NO:541, b is an integer of 15 to 1743, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:541, and where b is greater than or equal to a + 14.	H39746, H38765, H53680, H84385, H84386, H95751, H96427, H96428, N22709, N24033, N27417, N27531, N31183, N34699, N35427, N40348, N46995, N47385, W47664, W52613, W58021, AA020909, AA032219, AA032277, AA036745, AA053732, AA055872, AA057318, AA062713, AA070398, AA134055, AA132315, AA132625, AA149601, AA149602, AA494458, AA516430, AA534386, AA582804, AA581987, AA588838, AA631158, AA635970, AA577392, AA577494, AA857008, AA894813, AA933084, AI000994, N47386, D11495, D11593, D12071, D11877, D11882, D11902, AA456436, AA683214, AA890528, AA983938, AI074406, AI084728
841241	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 2196 of SEQ ID NO:542, b is an integer of 15 to 2210, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:542, and where b is greater than or equal to a + 14.	T64820, R18486, R48571, R48670, R51358, R51464, R70428, R71854, R77389, R77390, H18251, H18293, H18401, H18402, H19764, H19765, H21210, H21526, H24560, H25150, H26985, H28104, H30240, H30297, H30868, H30871, H40890, H41878, H41879, H43721, H43811, H43814,

		R84543, R85932, R87323, R93828, H49042, H49101, H51175, H51188, H68511, H75818, H80551, H80607, N41005, N45017, N56601, N70611, N74891, N93043, N93044, N94350, N98497, W04932, W21511, W21512, W24020, W31043, W47411, W47607, W47659, W47660, W48851, W48618, W52281, W56619, W56649, W68334, W68375, W70156, W70195, W84467, W84552, W90400, W94826, W96342, W96343, N91167, AA016293, AA017674, AA025151, AA025152, AA027955, AA031264, AA031395, AA031855, AA031854, AA035782, AA037318, AA040025, AA056359, AA069269, AA069418, AA069509, AA101608, AA114873, AA114837, AA115697, AA133516, AA220968, AA458530, AA460966, AA463596, AA419091, AA428836, AA507951, AA582836, AA640114, AA659114, AA836669, AA903136, AA903220, AA918099, AA928492, AA971856, AA973427, AA994099, AI016016, AI057267, AA069497, AA206877, AA218868, AA284783, AA284712, AA293434, AA293042, AA402851, AA454608, AA496283, AA609652, AA708123, AA757619, AA757695, AA774425, AA774630, AA775465, AA852435, AA852436, AA852604, AA852605, AA868271, AA884190, T03362, AI042345, AI042606, AI066399, AI086541, AI086967, AI091380, AI091725, AI092820, AI092945, T23722, F03416, F04814, F07127, F08608, F12341
841259	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1701 of SEQ ID NO:543, b is an integer of 15 to 1715, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:543, and where b is greater than or equal to a + 14.	
841260	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 3095 of SEQ ID NO:544, b is an integer of 15 to 3109, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:544, and where b is greater than or equal to a + 14.	T93673, R01175, R01287, R72262, R72263, H53584, H53905, N57686, N59657, N63715, N98804, W86302, W86653, W87312, AA055614, AA058962, AA058961, AA149239, AA180323, AA460554, AA460555, AA492261, AA596073, AA604012, AA612811, AA617927, AA631804, AA767954, AA769298, AA804811, AA814647, AA833776, AA872768, AA873458, AA876551, AA886069,

		AA932445. AA976417, AA989268, AI055853. D80933. AI088938. AI096484. AA215901, AA393250, AA435612, AA449044, AA449758. AA653318. AA678103, AA678744, AA705036, AA854081, AA789188, AA813062, AA868902, AI023192, AI033456. AI090508. Z28555, T25877. D30980, D31048. D31377. F00724, AA682530. AA694353
841264	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1162 of SEQ ID NO:545, b is an integer of 15 to 1176, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:545, and where b is greater than or equal to a + 14.	
841275	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1721 of SEQ ID NO:546, b is an integer of 15 to 1735, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:546, and where b is greater than or equal to a + 14.	
841311	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1034 of SEQ ID NO:547, b is an integer of 15 to 1048, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:547, and where b is greater than or equal to a + 14.	
841313	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 722 of SEQ ID NO:548, b is an integer of 15 to 736, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:548, and where b is greater than or equal to a + 14.	
841317	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 2217 of SEQ ID NO:549, b is an integer of 15 to 2231, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:549, and where b is greater than or equal to a + 14.	T78127, R31279, R31890, R38014, R68187, R68186, R68960, R81444, R81647, H03085, H42975, N22228, N35405, N40226, N52138, N66461, N66470, W48764, W49783, W58388, AA044222, AA044341, AA131687, AA131731, AA224224, AA224527, AA469092, AA580878, AA573581, AA863153, AA903745, AA971415, C03879, AA249392, AA448556, AA449703, F22605. AA723322, AA904943, Z18868, AA971554, AA991799, AI015846, AI037913, AI056007. AI082497, AI090170, AI095394

841322	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1802 of SEQ ID NO:550, b is an integer of 15 to 1816, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:550, and where b is greater than or equal to a + 14.	R21970, R83459, H65911, W76286, AA182592, AA281797, AA281874, AA291943, H65824, AA580660, AA748474, AA829390, AA293389, AA401755, AA910004, AA994494, AI005165, AI081877
841331	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 2596 of SEQ ID NO:551, b is an integer of 15 to 2610, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:551, and where b is greater than or equal to a + 14.	
841332	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 4007 of SEQ ID NO:552, b is an integer of 15 to 4021, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:552, and where b is greater than or equal to a + 14.	
841338	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1766 of SEQ ID NO:553, b is an integer of 15 to 1780, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:553, and where b is greater than or equal to a + 14.	
841345	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 3699 of SEQ ID NO:554, b is an integer of 15 to 3713, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:554, and where b is greater than or equal to a + 14.	
841349	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1983 of SEQ ID NO:555, b is an integer of 15 to 1997, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:555, and where b is greater than or equal to a + 14.	
841355	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 892 of SEQ ID NO:556, b is an integer of 15 to 906, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:556, and where b is greater than or equal to a + 14.	
841417	Preferably excluded from the present invention are	

	one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 3470 of SEQ ID NO:557, b is an integer of 15 to 3484, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:557, and where b is greater than or equal to a + 14.	
841548	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 776 of SEQ ID NO:558, b is an integer of 15 to 790, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:558, and where b is greater than or equal to a + 14.	AA223588
841632	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 544 of SEQ ID NO:559, b is an integer of 15 to 558, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:559, and where b is greater than or equal to a + 14.	
841662	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 520 of SEQ ID NO:560, b is an integer of 15 to 534, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:560, and where b is greater than or equal to a + 14.	H15850, H99706, N78646, W74702, W94916, AA809695
841771	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 3029 of SEQ ID NO:561, b is an integer of 15 to 3043, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:561, and where b is greater than or equal to a + 14.	T50029, T67900, T74699, T74819, T88802, T81298, T84439, T95656, R06092, R06196, R14563, R14966, R14970, R16465, R38948, R40957, R40957, R63975, R64085, R66362, R66363, R67505, H17644, H17758, R92097, H48240, H48331, H49625, H49715, H61167, H62068, H69147, N25753, N36472, N69035, N71493, N92970, N98567, N99536, W00665, W24251, W40582, W45462, W45538, W45525, W45687, W44315, W57971, W57944, W70012, W70013, W86733, AA044684, AA071192, AA071199, AA190325, AA191520, AA533197, AA558210, AA581106, AA581161, AA577119, AA857551, AA878885, AA936839, AA975697, D78980, W28535, C02075, C17857
841827	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1372 of SEQ ID NO:562, b is an integer of 15 to 1386, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:562, and where b is	

	greater than or equal to a + 14.	
841835	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 2624 of SEQ ID NO:563, b is an integer of 15 to 2638, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:563, and where b is greater than or equal to a + 14.	
842259	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 677 of SEQ ID NO:564, b is an integer of 15 to 691, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:564, and where b is greater than or equal to a + 14.	
842463	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1953 of SEQ ID NO:565, b is an integer of 15 to 1967, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:565, and where b is greater than or equal to a + 14.	
842595	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1320 of SEQ ID NO:566, b is an integer of 15 to 1334, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:566, and where b is greater than or equal to a + 14.	
842722	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1596 of SEQ ID NO:567, b is an integer of 15 to 1610, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:567, and where b is greater than or equal to a + 14.	
842815	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1398 of SEQ ID NO:568, b is an integer of 15 to 1412, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:568, and where b is greater than or equal to a + 14.	
842818	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1111 of SEQ ID NO:569, b is an integer of 15 to 1125, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:569, and where b is greater than or equal to a + 14.	

843251	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1902 of SEQ ID NO:570, b is an integer of 15 to 1916, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:570, and where b is greater than or equal to a + 14.	
843422	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1239 of SEQ ID NO:571, b is an integer of 15 to 1253, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:571, and where b is greater than or equal to a + 14.	
843784	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1999 of SEQ ID NO:572, b is an integer of 15 to 2013, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:572, and where b is greater than or equal to a + 14.	
844017	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 655 of SEQ ID NO:573, b is an integer of 15 to 669, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:573, and where b is greater than or equal to a + 14.	AA075932
844138	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 2418 of SEQ ID NO:574, b is an integer of 15 to 2432, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:574, and where b is greater than or equal to a + 14.	T54096, T54187, T54360, T39143, T40432, T90493, T90589, T89428, T89794, T80000, R00221, R00327, R25952, R26450, R26761, R28459, R55293, R55390, R73233, H42630, H44454, H44498, R83525, R86282, H85785, N33586, N34419, N36244, N48653, N49430, W51915, AA055530, AA055939, AA069732, AA100817, AA122084, AA121407, AA126332, AA133329, AA134151, AA134152, AA134714, AA136470, AA136960, AA157850, AA157906, AA157976, AA159365, AA171854, AA187219, AA186342, AA250818, AA464565, AA464666, AA428826, AA429361, AA491863, AA505512, AA524490, AA558038, AA581979, AA588712, AA593885, AA601110, AA573930, AA577156, AA578735, AA689519, AA730155, AA768486, AA805061, AA826981, AA865985, AA931167, AA947324, AA953202, AA961105, AA962413, AA976440, AA977760, AI032134, AI053416, AI053575,

		AI054013, AI054146, AI054281, U46376, W22126, C00371, C05283, AA641416, AA643346, AA292261, AA421818, AA496452, AA496521, AA653437, AA664399, AA680123, AA431832, AA434143, AA678582, AA705952, AA679763, AA733019, AA781645, AA813232, AA833597, AA844624, AI024151, AI038232, AI042551, AI080152, AI086490, T24101, F03522, F07244
844166	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1358 of SEQ ID NO:575, b is an integer of 15 to 1372, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:575, and where b is greater than or equal to a + 14.	
844194	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 2006 of SEQ ID NO:576, b is an integer of 15 to 2020, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:576, and where b is greater than or equal to a + 14.	
844394	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 3147 of SEQ ID NO:577, b is an integer of 15 to 3161, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:577, and where b is greater than or equal to a + 14.	
844450	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 2032 of SEQ ID NO:578, b is an integer of 15 to 2046, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:578, and where b is greater than or equal to a + 14.	
844534	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 288 of SEQ ID NO:579, b is an integer of 15 to 302, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:579, and where b is greater than or equal to a + 14.	
844535	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 3053 of SEQ ID NO:580, b is an integer of 15 to 3067, where both a and b correspond to the positions of nucleotide	

	residues shown in SEQ ID NO:580, and where b is greater than or equal to a + 14.	
844644	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1560 of SEQ ID NO:581, b is an integer of 15 to 1574, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:581, and where b is greater than or equal to a + 14.	
844653	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 946 of SEQ ID NO:582, b is an integer of 15 to 960, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:582, and where b is greater than or equal to a + 14.	
844659	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 527 of SEQ ID NO:583, b is an integer of 15 to 541, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:583, and where b is greater than or equal to a + 14.	
844796	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 2954 of SEQ ID NO:584, b is an integer of 15 to 2968, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:584, and where b is greater than or equal to a + 14.	
844812	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 2594 of SEQ ID NO:585, b is an integer of 15 to 2608, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:585, and where b is greater than or equal to a + 14.	
844894	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1879 of SEQ ID NO:586, b is an integer of 15 to 1893, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:586, and where b is greater than or equal to a + 14.	
845361	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 2449 of SEQ ID NO:587, b is an integer of 15 to 2463, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:587, and where b is	T93072, T93161, T69748, T70732, R01200, R01312, R05457, R05477, R05584, R43190, R43190, R65942, R75719, R78234, H03875, H03876, H15845, H16155, H17787, H40269, H45881, R84787, R92493, R92931, H58301, H58912, H58913, H62257,

	greater than or equal to a + 14.	H67051, H68135, H81385, H83681, H91363, H96711, N20348, N22509, N27952, N28616, N31997, N32005, N36007, N39356, N40718, N70011, N70094, N92576, N99870, W00896, W00925, W04623, W25220, W31522, W37278, W37791, W38868, W52654, W51751, AA017158, AA019458, AA022914, AA022915, AA037370, AA037502, AA045696, AA045697, AA046013, AA054565, AA054625, AA069778, AA079736, AA081087, AA081144, AA100055, AA100504, AA100334, AA115581, AA115554, AA126149, AA126373, AA133101, AA130558, AA136439, AA151673, AA151821, AA151822, AA159031, AA165200, AA165201, AA176477, AA176498, AA176771, AA176830, AA182601, AA176736, AA187943, AA188578, AA188675, AA190342, AA190343, AA195091, AA213662, AA213715, AA232222, AA426516, AA424760, AA483564, AA490859, AA491042, AA505249, AA507988, AA508858, AA513433, AA514771, AA514785, AA514980, AA527545, AA534100, AA554008, AA557148, AA584946, AA586481, AA587849, AA588781, AA593916, AA605049, AA604893, AA617650, AA568567, AA621979, AA627588, AA578585, AA578744, AA661910, AA729355, AA729902, AA736994, AA738388, AA740375, AA741213, AA760943, AA830401, AA834201, AA834208, AA834250, AA864864, AA888527, AA906940, AA922073, AA927272, AA931625, AA933055, AA932772, AA936861, AA938504, AA975187, AA977857, AA975594, AI000724, AI014600, AI017381, AI066441, D82733, U47688, N83708, N83790, N85010, W22533, W23255, N86314, N87393, N88971, AA642249, AA642903, AA090403, AA091011, AA095990, AA205824, AA204931, AA643262, AA648446, AA216706, AA219615, AA249170, C75338, AA599187, AA668746, AA670340, AA405611, AA405150, AA708635, AA716044, AA722076, AA722829, AA725716, AA781064, AA844379, AI037987, AI039577, AI078722, AI077655, AI080306, AI084320, AI085219, AI093296, AI093479, AI095168, AI095267, D29018, F02782,

		F06502, F00762, F00966
845620	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1931 of SEQ ID NO:588, b is an integer of 15 to 1945, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:588, and where b is greater than or equal to a + 14.	
845639	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 802 of SEQ ID NO:589, b is an integer of 15 to 816, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:589, and where b is greater than or equal to a + 14.	
845660	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 2293 of SEQ ID NO:590, b is an integer of 15 to 2307, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:590, and where b is greater than or equal to a + 14.	
845720	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1424 of SEQ ID NO:591, b is an integer of 15 to 1438, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:591, and where b is greater than or equal to a + 14.	
845785	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1064 of SEQ ID NO:592, b is an integer of 15 to 1078, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:592, and where b is greater than or equal to a + 14.	
845897	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 2478 of SEQ ID NO:593, b is an integer of 15 to 2492, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:593, and where b is greater than or equal to a + 14.	
845922	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1890 of SEQ ID NO:594, b is an integer of 15 to 1904, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:594, and where b is greater than or equal to a + 14.	

846016	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 323 of SEQ ID NO:595, b is an integer of 15 to 337, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:595, and where b is greater than or equal to a + 14.	
846040	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1274 of SEQ ID NO:596, b is an integer of 15 to 1288, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:596, and where b is greater than or equal to a + 14.	
846073	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1038 of SEQ ID NO:597, b is an integer of 15 to 1052, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:597, and where b is greater than or equal to a + 14.	T83567, T83771, R51147, N26938, N32715, N36666, W57781, W74108, AA082091, AA425613
846257	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 2079 of SEQ ID NO:598, b is an integer of 15 to 2093, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:598, and where b is greater than or equal to a + 14.	

Polynucleotide and Polypeptide Variants

The present invention is directed to variants of the polynucleotide sequence disclosed in SEQ ID NO:X or the complementary strand thereto, and/or the cDNA sequence contained in a cDNA clone contained in the deposit.

The present invention also encompasses variants of the cancer polypeptide sequence disclosed in SEQ ID NO:Y, a polypeptide sequence encoded by the polynucleotide sequence in SEQ ID NO:X, and/or a polypeptide sequence encoded by the cDNA in the related cDNA clone contained in the deposit.

"Variant" refers to a polynucleotide or polypeptide differing from the polynucleotide or polypeptide of the present invention, but retaining essential properties thereof. Generally, variants are overall closely similar, and, in many regions, identical to the polynucleotide or polypeptide of the present invention.

The present invention is also directed to nucleic acid molecules which comprise, or alternatively consist of, a nucleotide sequence which is at least 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99% or 100%, identical to, for example, the nucleotide coding sequence in SEQ ID NO:X or the complementary strand thereto, the nucleotide coding sequence of the related cDNA contained in a deposited library or the complementary strand thereto, a nucleotide sequence encoding the polypeptide of SEQ ID NO:Y, a nucleotide sequence encoding a polypeptide sequence encoded by the nucleotide sequence in SEQ ID NO:X, a nucleotide sequence encoding the polypeptide encoded by the cDNA in the related cDNA contained in a deposited library, and/or polynucleotide fragments of any of these nucleic acid molecules (e.g., those fragments described herein). Polypeptides encoded by these nucleic acid molecules are also encompassed by the invention. In another embodiment, the invention encompasses nucleic acid molecules which comprise or alternatively consist of, a polynucleotide which hybridizes under stringent hybridization conditions, or alternatively, under low stringency conditions, to the nucleotide coding sequence in SEQ ID NO:X, the nucleotide coding sequence of the related cDNA clone contained in a deposited library, a nucleotide sequence encoding the polypeptide of SEQ ID NO:Y, a nucleotide sequence encoding a polypeptide sequence encoded by the nucleotide sequence in SEQ ID NO:X, a nucleotide sequence encoding the polypeptide encoded by the cDNA in the related cDNA clone contained in a deposited library, and/or polynucleotide fragments of any of these nucleic acid molecules (e.g., those fragments described herein). Polynucleotides which

hybridize to the complement of these nucleic acid molecules under stringent hybridization conditions or alternatively, under lower stringency conditions, are also encompassed by the invention, as are polypeptides encoded by these polynucleotides.

The present invention is also directed to polypeptides which comprise, or alternatively consist of, an amino acid sequence which is at least 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99% or 100% identical to, for example, the polypeptide sequence shown in SEQ ID NO:Y, a polypeptide sequence encoded by the nucleotide sequence in SEQ ID NO:X, a polypeptide sequence encoded by the cDNA in the related cDNA clone contained in a deposited library, and/or polypeptide fragments of any of these polypeptides (e.g., those fragments described herein). Polynucleotides which hybridize to the complement of the nucleic acid molecules encoding these polypeptides under stringent hybridization conditions, or alternatively, under lower stringency conditions, are also encompassed by the invention, as are polypeptides encoded by these polynucleotides.

By a nucleic acid having a nucleotide sequence at least, for example, 95% "identical" to a reference nucleotide sequence of the present invention, it is intended that the nucleotide sequence of the nucleic acid is identical to the reference sequence except that the nucleotide sequence may include up to five point mutations per each 100 nucleotides of the reference nucleotide sequence encoding the polypeptide. In other words, to obtain a nucleic acid having a nucleotide sequence at least 95% identical to a reference nucleotide sequence, up to 5% of the nucleotides in the reference sequence may be deleted or substituted with another nucleotide, or a number of nucleotides up to 5% of the total nucleotides in the reference sequence may be inserted into the reference sequence. The query sequence may be, for example, an entire sequence referred to in Table 1, an ORF (open reading frame), or any fragment specified as described herein.

As a practical matter, whether any particular nucleic acid molecule or polypeptide is at least 80%, 85%, 90%, 95%, 96%, 97%, 98% or 99% identical to a nucleotide sequence of the present invention can be determined conventionally using known computer programs. A preferred method for determining the best overall match between a query sequence (a sequence of the present invention) and a subject sequence, also referred to as a global sequence alignment, can be determined using the FASTDB computer program based on the algorithm of Brutlag et al. (Comp. App. Biosci. 6:237-245 (1990)). In a sequence alignment the query and subject sequences are both DNA sequences. An RNA sequence can be

compared by converting U's to T's. The result of said global sequence alignment is in percent identity. Preferred parameters used in a FASTDB alignment of DNA sequences to calculate percent identiy are: Matrix=Unitary, k-tuple=4, Mismatch Penalty=1, Joining Penalty=30, Randomization Group Length=0, Cutoff Score=1, Gap Penalty=5, Gap Size Penalty 0.05, Window Size=500 or the lenght of the subject nucleotide sequence, whichever is shorter.

If the subject sequence is shorter than the query sequence because of 5' or 3' deletions, not because of internal deletions, a manual correction must be made to the results. This is because the FASTDB program does not account for 5' and 3' truncations of the subject sequence when calculating percent identity. For subject sequences truncated at the 5' or 3' ends, relative to the query sequence, the percent identity is corrected by calculating the number of bases of the query sequence that are 5' and 3' of the subject sequence, which are not matched/aligned, as a percent of the total bases of the query sequence. Whether a nucleotide is matched/aligned is determined by results of the FASTDB sequence alignment. This percentage is then subtracted from the percent identity, calculated by the above FASTDB program using the specified parameters, to arrive at a final percent identity score. This corrected score is what is used for the purposes of the present invention. Only bases outside the 5' and 3' bases of the subject sequence, as displayed by the FASTDB alignment, which are not matched/aligned with the query sequence, are calculated for the purposes of manually adjusting the percent identity score.

For example, a 90 base subject sequence is aligned to a 100 base query sequence to determine percent identity. The deletions occur at the 5' end of the subject sequence and therefore, the FASTDB alignment does not show a matched/alignment of the first 10 bases at 5' end. The 10 unpaired bases represent 10% of the sequence (number of bases at the 5' and 3' ends not matched/total number of bases in the query sequence) so 10% is subtracted from the percent identity score calculated by the FASTDB program. If the remaining 90 bases were perfectly matched the final percent identity would be 90%. In another example, a 90 base subject sequence is compared with a 100 base query sequence. This time the deletions are internal deletions so that there are no bases on the 5' or 3' of the subject sequence which are not matched/aligned with the query. In this case the percent identity calculated by FASTDB is not manually corrected. Once again, only bases 5' and 3' of the subject sequence which are not matched/aligned with the query sequence are manually corrected for. No other

manual corrections are to made for the purposes of the present invention.

By a polypeptide having an amino acid sequence at least, for example, 95% "identical" to a query amino acid sequence of the present invention, it is intended that the amino acid sequence of the subject polypeptide is identical to the query sequence except that the subject polypeptide sequence may include up to five amino acid alterations per each 100 amino acids of the query amino acid sequence. In other words, to obtain a polypeptide having an amino acid sequence at least 95% identical to a query amino acid sequence, up to 5% of the amino acid residues in the subject sequence may be inserted, deleted, (indels) or substituted with another amino acid. These alterations of the reference sequence may occur at the amino or carboxy terminal positions of the reference amino acid sequence or anywhere between those terminal positions, interspersed either individually among residues in the reference sequence or in one or more contiguous groups within the reference sequence.

As a practical matter, whether any particular polypeptide is at least 80%, 85%, 90%, 95%, 96%, 97%, 98% or 99% identical to, for instance, the amino acid sequence in SEQ ID NO:Y or a fragment thereof, the amino acid sequence encoded by the nucleotide sequence in SEQ ID NO:X or a fragment thereof, or the amino acid sequence encoded by the cDNA in the related cDNA clone contained in a deposited library, or a fragment thereof, can be determined conventionally using known computer programs. A preferred method for determing the best overall match between a query sequence (a sequence of the present invention) and a subject sequence, also referred to as a global sequence alignment, can be determined using the FASTDB computer program based on the algorithm of Brutlag et al. (Comp. App. Biosci.6:237- 245(1990)). In a sequence alignment the query and subject sequences are either both nucleotide sequences or both amino acid sequences. The result of said global sequence alignment is in percent identity. Preferred parameters used in a FASTDB amino acid alignment are: Matrix=PAM 0, k-tuple=2, Mismatch Penalty=1, Joining Penalty=20, Randomization Group Length=0, Cutoff Score=1, Window Size=sequence length, Gap Penalty=5, Gap Size Penalty=0.05, Window Size=500 or the length of the subject amino acid sequence, whichever is shorter.

If the subject sequence is shorter than the query sequence due to N- or C-terminal deletions, not because of internal deletions, a manual correction must be made to the results. This is because the FASTDB program does not account for N- and C-terminal truncations of the subject sequence when calculating global percent identity. For subject sequences

truncated at the N- and C-termini, relative to the query sequence, the percent identity is corrected by calculating the number of residues of the query sequence that are N- and C-terminal of the subject sequence, which are not matched/aligned with a corresponding subject residue, as a percent of the total bases of the query sequence. Whether a residue is matched/aligned is determined by results of the FASTDB sequence alignment. This percentage is then subtracted from the percent identity, calculated by the above FASTDB program using the specified parameters, to arrive at a final percent identity score. This final percent identity score is what is used for the purposes of the present invention. Only residues to the N- and C-termini of the subject sequence, which are not matched/aligned with the query sequence, are considered for the purposes of manually adjusting the percent identity score. That is, only query residue positions outside the farthest N- and C- terminal residues of the subject sequence.

For example, a 90 amino acid residue subject sequence is aligned with a 100 residue query sequence to determine percent identity. The deletion occurs at the N-terminus of the subject sequence and therefore, the FASTDB alignment does not show a matching/alignment of the first 10 residues at the N-terminus. The 10 unpaired residues represent 10% of the sequence (number of residues at the N- and C- termini not matched/total number of residues in the query sequence) so 10% is subtracted from the percent identity score calculated by the FASTDB program. If the remaining 90 residues were perfectly matched the final percent identity would be 90%. In another example, a 90 residue subject sequence is compared with a 100 residue query sequence. This time the deletions are internal deletions so there are no residues at the N- or C-termini of the subject sequence which are not matched/aligned with the query. In this case the percent identity calculated by FASTDB is not manually corrected. Once again, only residue positions outside the N- and C-terminal ends of the subject sequence, as displayed in the FASTDB alignment, which are not matched/aligned with the query sequence are manually corrected for. No other manual corrections are to made for the purposes of the present invention.

The variants may contain alterations in the coding regions, non-coding regions, or both. Especially preferred are polynucleotide variants containing alterations which produce silent substitutions, additions, or deletions, but do not alter the properties or activities of the encoded polypeptide. Nucleotide variants produced by silent substitutions due to the degeneracy of the genetic code are preferred. Moreover, variants in which less than 50, less

than 40, less than 30, less than 20, less than 10, or 5-50, 5-25, 5-10, 1-5, or 1-2 amino acids are substituted, deleted, or added in any combination are also preferred. Polynucleotide variants can be produced for a variety of reasons, e.g., to optimize codon expression for a particular host (change codons in the human mRNA to those preferred by a bacterial host such as E. coli).

Naturally occurring variants are called "allelic variants," and refer to one of several alternate forms of a gene occupying a given locus on a chromosome of an organism. (Genes II, Lewin, B., ed., John Wiley & Sons, New York (1985).) These allelic variants can vary at either the polynucleotide and/or polypeptide level and are included in the present invention. Alternatively, non-naturally occurring variants may be produced by mutagenesis techniques or by direct synthesis.

Using known methods of protein engineering and recombinant DNA technology, variants may be generated to improve or alter the characteristics of the polypeptides of the present invention. For instance, as discussed herein, one or more amino acids can be deleted from the N-terminus or C-terminus of the polypeptide of the present invention without substantial loss of biological function. The authors of Ron et al., J. Biol. Chem. 268: 2984-2988 (1993), reported variant KGF proteins having heparin binding activity even after deleting 3, 8, or 27 amino-terminal amino acid residues. Similarly, Interferon gamma exhibited up to ten times higher activity after deleting 8-10 amino acid residues from the carboxy terminus of this protein. (Dobeli et al., J. Biotechnology 7:199-216 (1988).)

Moreover, ample evidence demonstrates that variants often retain a biological activity similar to that of the naturally occurring protein. For example, Gayle and coworkers (J. Biol. Chem 268:22105-22111 (1993)) conducted extensive mutational analysis of human cytokine IL-1a. They used random mutagenesis to generate over 3,500 individual IL-1a mutants that averaged 2.5 amino acid changes per variant over the entire length of the molecule. Multiple mutations were examined at every possible amino acid position. The investigators found that "[m]ost of the molecule could be altered with little effect on either [binding or biological activity]." (See, Abstract.) In fact, only 23 unique amino acid sequences, out of more than 3,500 nucleotide sequences examined, produced a protein that significantly differed in activity from wild-type.

Furthermore, as discussed herein, even if deleting one or more amino acids from the N-terminus or C-terminus of a polypeptide results in modification or loss of one or more

biological functions, other biological activities may still be retained. For example, the ability of a deletion variant to induce and/or to bind antibodies which recognize the secreted form will likely be retained when less than the majority of the residues of the secreted form are removed from the N-terminus or C-terminus. Whether a particular polypeptide lacking N- or C-terminal residues of a protein retains such immunogenic activities can readily be determined by routine methods described herein and otherwise known in the art.

Thus, the invention further includes polypeptide variants which show a functional activity (e.g., biological activity) of the polypeptide of the invention of which they are a variant. Such variants include deletions, insertions, inversions, repeats, and substitutions selected according to general rules known in the art so as have little effect on activity.

The present application is directed to nucleic acid molecules at least 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99% or 100% identical to the nucleic acid sequences disclosed herein or fragments thereof, (e.g., including but not limited to fragments encoding a polypeptide having the amino acid sequence of an N and/or C terminal deletion), irrespective of whether they encode a polypeptide having functional activity. This is because even where a particular nucleic acid molecule does not encode a polypeptide having functional activity, one of skill in the art would still know how to use the nucleic acid molecule, for instance, as a hybridization probe or a polymerase chain reaction (PCR) primer. Uses of the nucleic acid molecules of the present invention that do not encode a polypeptide having functional activity include, inter alia, (1) isolating a gene or allelic or splice variants thereof in a cDNA library; (2) in situ hybridization (e.g., "FISH") to metaphase chromosomal spreads to provide precise chromosomal location of the gene, as described in Verma et al., Human Chromosomes: A Manual of Basic Techniques, Pergamon Press, New York (1988); and (3) Northern Blot analysis for detecting mRNA expression in specific tissues.

Preferred, however, are nucleic acid molecules having sequences at least 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99% or 100% identical to the nucleic acid sequences disclosed herein, which do, in fact, encode a polypeptide having a functional activity of a polypeptide of the invention.

Of course, due to the degeneracy of the genetic code, one of ordinary skill in the art will immediately recognize that a large number of the nucleic acid molecules having a sequence at least 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, or 100% identical to, for example, the nucleic acid sequence of the cDNA in the related cDNA clone contained in a

deposited library, the nucleic acid sequence referred to in Table 1 (SEQ ID NO:X), or fragments thereof, will encode polypeptides "having functional activity." In fact, since degenerate variants of any of these nucleotide sequences all encode the same polypeptide, in many instances, this will be clear to the skilled artisan even without performing the above described comparison assay. It will be further recognized in the art that, for such nucleic acid molecules that are not degenerate variants, a reasonable number will also encode a polypeptide having functional activity. This is because the skilled artisan is fully aware of amino acid substitutions that are either less likely or not likely to significantly effect protein function (e.g., replacing one aliphatic amino acid with a second aliphatic amino acid), as further described below.

For example, guidance concerning how to make phenotypically silent amino acid substitutions is provided in Bowie et al., "Deciphering the Message in Protein Sequences: Tolerance to Amino Acid Substitutions," Science 247:1306-1310 (1990), wherein the authors indicate that there are two main strategies for studying the tolerance of an amino acid sequence to change.

The first strategy exploits the tolerance of amino acid substitutions by natural selection during the process of evolution. By comparing amino acid sequences in different species, conserved amino acids can be identified. These conserved amino acids are likely important for protein function. In contrast, the amino acid positions where substitutions have been tolerated by natural selection indicates that these positions are not critical for protein function. Thus, positions tolerating amino acid substitution could be modified while still maintaining biological activity of the protein.

The second strategy uses genetic engineering to introduce amino acid changes at specific positions of a cloned gene to identify regions critical for protein function. For example, site directed mutagenesis or alanine-scanning mutagenesis (introduction of single alanine mutations at every residue in the molecule) can be used. (Cunningham and Wells, Science 244:1081-1085 (1989).) The resulting mutant molecules can then be tested for biological activity.

As the authors state, these two strategies have revealed that proteins are surprisingly tolerant of amino acid substitutions. The authors further indicate which amino acid changes are likely to be permissive at certain amino acid positions in the protein. For example, most buried (within the tertiary structure of the protein) amino acid residues require nonpolar side

chains, whereas few features of surface side chains are generally conserved. Moreover, tolerated conservative amino acid substitutions involve replacement of the aliphatic or hydrophobic amino acids Ala, Val, Leu and Ile; replacement of the hydroxyl residues Ser and Thr; replacement of the acidic residues Asp and Glu; replacement of the amide residues Asn and Gln, replacement of the basic residues Lys, Arg, and His; replacement of the aromatic residues Phe, Tyr, and Trp, and replacement of the small-sized amino acids Ala, Ser, Thr, Met, and Gly. Besides conservative amino acid substitution, variants of the present invention include (i) substitutions with one or more of the non-conserved amino acid residues, where the substituted amino acid residues may or may not be one encoded by the genetic code, or (ii) substitution with one or more of amino acid residues having a substituent group, or (iii) fusion of the mature polypeptide with another compound, such as a compound to increase the stability and/or solubility of the polypeptide (for example, polyethylene glycol), or (iv) fusion of the polypeptide with additional amino acids, such as, for example, an IgG Fc fusion region peptide, or leader or secretory sequence, or a sequence facilitating purification. Such variant polypeptides are deemed to be within the scope of those skilled in the art from the teachings herein.

For example, polypeptide variants containing amino acid substitutions of charged amino acids with other charged or neutral amino acids may produce proteins with improved characteristics, such as less aggregation. Aggregation of pharmaceutical formulations both reduces activity and increases clearance due to the aggregate's immunogenic activity. (Pinckard et al., Clin. Exp. Immunol. 2:331-340 (1967); Robbins et al., Diabetes 36: 838-845 (1987); Cleland et al., Crit. Rev. Therapeutic Drug Carrier Systems 10:307-377 (1993).)

A further embodiment of the invention relates to a polypeptide which comprises the amino acid sequence of a polypeptide having an amino acid sequence which contains at least one amino acid substitution, but not more than 50 amino acid substitutions, even more preferably, not more than 40 amino acid substitutions, still more preferably, not more than 30 amino acid substitutions, and still even more preferably, not more than 20 amino acid substitutions. Of course it is highly preferable for a polypeptide to have an amino acid sequence which comprises the amino acid sequence of a polypeptide of SEQ ID NO:Y, an amino acid sequence encoded by SEQ ID NO:X, and/or the amino acid sequence encoded by the cDNA in the related cDNA clone contained in a deposited library which contains, in order of ever-increasing preference, at least one, but not more than 10, 9, 8, 7, 6, 5, 4, 3, 2 or 1

amino acid substitutions. In specific embodiments, the number of additions, substitutions, and/or deletions in the amino acid sequence of SEQ ID NO:Y or fragments thereof (e.g., the mature form and/or other fragments described herein), an amino acid sequence encoded by SEQ ID NO:X or fragments thereof, and/or the amino acid sequence encoded by the cDNA in the related cDNA clone contained in a deposited library or fragments thereof, is 1-5, 5-10, 5-25, 5-50, 10-50 or 50-150, conservative amino acid substitutions are preferable.

Polynucleotide and Polypeptide Fragments

The present invention is also directed to polynucleotide fragments of the cancer polynucleotides (nucleic acids) of the invention. In the present invention, a "polynucleotide fragment" refers, for example, to a polynucleotide having a nucleic acid sequence which: is a portion of the cDNA contained in a depostied cDNA clone; or is a portion of a polynucleotide sequence encoding the polypeptide encoded by the cDNA contained in a deposited cDNA clone; or is a portion of the polynucleotide sequence in SEQ ID NO:X or the complementary strand thereto; or is a polynucleotide sequence encoding a portion of the polypeptide of SEQ ID NO:Y; or is a polynucleotide sequence encoding a portion of a polypeptide encoded by SEQ ID NO:X or the complementary strand thereto. The nucleotide fragments of the invention are preferably at least about 15 nt, and more preferably at least about 20 nt, still more preferably at least about 30 nt, and even more preferably, at least about 40 nt, at least about 50 nt; at least about 75 nt, at least about 100 nt, at least about 125 nt or at least about 150 nt in length. A fragment "at least 20 nt in length," for example, is intended to include 20 or more contiguous bases from, for example, the sequence contained in the cDNA in a related cDNA clone contained in a deposited library, the nucleotide sequence shown in SEQ ID NO:X or the complementary stand thereto. In this context “about” includes the particularly recited value or a value larger or smaller by several (5, 4, 3, 2, or 1) nucleotides. These nucleotide fragments have uses that include, but are not limited to, as diagnostic probes and primers as discussed herein. Of course, larger fragments (e.g., at least 150, 175, 200, 250, 500, 600, 1000, or 2000 nucleotides in length) are also encompassed by the invention.

Moreover, representative examples of polynucleotide fragments of the invention, include, for example, fragments comprising, or alternatively consisting of, a sequence from about nucleotide number 1-50, 51-100, 101-150, 151-200, 201-250, 251-300, 301-350, 351-400, 401-450, 451-500, 501-550, 551-600, 651-700,701- 750, 751-800, 800-850, 851-900,

901-950, 951-1000, 1001-1050, 1051-1100, 1101-1150, 1151-1200, 1201-1250, 1251-1300, 1301-1350, 1351-1400, 1401-1450, 1451-1500, 1501-1550, 1551-1600, 1601-1650, 1651-1700, 1701-1750, 1751-1800, 1801-1850, 1851-1900, 1901-1950, 1951-2000, 2001-2050, 2051-2100, 2101-2150, 2151-2200, 2201-2250, 2251-2300, 2301-2350, 2351-2400, 2401-2450, 2451-2500, 2501-2550, 2551-2600, 2601-2650, 2651-2700, 2701-2750, 2751-2800, 2801-2850, 2851-2900, 2901-2950, 2951-3000, 3001-3050, 3051-3100, 3101-3150, 3151-3200, 3201-3250, 3251-3300, 3301-3350, 3351-3400, 3401-3450, 3451-3500, 3501-3550, and 3551 to the end of SEQ ID NO:X, or the complementary strand thereto. In this context "about" includes the particularly recited range or a range larger or smaller by several (5, 4, 3, 2, or 1) nucleotides, at either terminus or at both termini. Preferably, these fragments encode a polypeptide which has a functional activity (e.g., biological activity) of the polypeptide encoded by the polynucleotide of which the sequence is a portion. More preferably, these fragments can be used as probes or primers as discussed herein. Polynucleotides which hybridize to one or more of these nucleic acid molecules under stringent hybridization conditions or alternatively, under lower stringency conditions, are also encompassed by the invention, as are polypeptides encoded by these polynucleotides or fragments.

Moreover, representative examples of polynucleotide fragments of the invention, include, for example, fragments comprising, or alternatively consisting of, a sequence from about nucleotide number 1-50, 51-100, 101-150, 151-200, 201-250, 251-300, 301-350, 351-400, 401-450, 451-500, 501-550, 551-600, 651-700,701- 750, 751-800, 800-850, 851-900, 901-950, 951-1000, 1001-1050, 1051-1100, 1101-1150, 1151-1200, 1201-1250, 1251-1300, 1301-1350, 1351-1400, 1401-1450, 1451-1500, 1501-1550, 1551-1600, 1601-1650, 1651-1700, 1701-1750, 1751-1800, 1801-1850, 1851-1900, 1901-1950, 1951-2000, 2001-2050, 2051-2100, 2101-2150, 2151-2200, 2201-2250, 2251-2300, 2301-2350, 2351-2400, 2401-2450, 2451-2500, 2501-2550, 2551-2600, 2601-2650, 2651-2700, 2701-2750, 2751-2800, 2801-2850, 2851-2900, 2901-2950, 2951-3000, 3001-3050, 3051-3100, 3101-3150, 3151-3200, 3201-3250, 3251-3300, 3301-3350, 3351-3400, 3401-3450, 3451-3500, 3501-3550, and 3551 to the end of the cDNA nucleotide sequence contained in the deposited cDNA clone, or the complementary strand thereto. In this context "about" includes the particularly recited range, or a range larger or smaller by several (5, 4, 3, 2, or 1) nucleotides, at either terminus or at both termini. Preferably, these fragments encode a polypeptide which has a functional activity (e.g., biological activity) of the polypeptide encoded by the cDNA

nucleotide sequence contained in the deposited cDNA clone. More preferably, these fragments can be used as probes or primers as discussed herein. Polynucleotides which hybridize to one or more of these fragments under stringent hybridization conditions or alternatively, under lower stringency conditions, are also encompassed by the invention, as are polypeptides encoded by these polynucleotides or fragments.

In the present invention, a "polypeptide fragment" refers to an amino acid sequence which is a portion of that contained in SEQ ID NO:Y, a portion of an amino acid sequence encoded by the polynucleotide sequence of SEQ ID NO:X, and/or encoded by the cDNA contained in the related cDNA clone contained in a deposited library. Protein (polypeptide) fragments may be "free-standing," or comprised within a larger polypeptide of which the fragment forms a part or region, most preferably as a single continuous region. Representative examples of polypeptide fragments of the invention, include, for example, fragments comprising, or alternatively consisting of, an amino acid sequence from about amino acid number 1-20, 21-40, 41-60, 61-80, 81-100, 102-120, 121-140, 141-160, 161-180, 181-200, 201-220, 221-240, 241-260, 261-280, 281-300, 301-320, 321-340, 341-360, 361-380, 381-400, 401-420, 421-440, 441-460, 461-480, 481-500, 501-520, 521-540, 541-560, 561-580, 581-600, 601-620, 621-640, 641-660, 661-680, 681-700, 701-720, 721-740, 741-760, 761-780, 781-800, 801-820, 821-840, 841-860, 861-880, 881-900, 901-920, 921-940, 941-960, 961-980, 981-1000, 1001-1020, 1021-1040, 1041-1060, 1061-1080, 1081-1100, 1101-1120, 1121-1140, 1141-1160, 1161-1180, and 1181 to the end of SEQ ID NO:Y. Moreover, polypeptide fragments of the invention may be at least about 10, 15, 20, 25, 30, 35, 40, 45, 50, 55, 60, 65, 70, 75, 80, 85, 90, 100, 110, 120, 130, 140, or 150 amino acids in length. In this context "about" includes the particularly recited ranges or values, or ranges or values larger or smaller by several (5, 4, 3, 2, or 1) amino acids, at either terminus or at both termini. Polynucleotides encoding these polypeptide fragments are also encompassed by the invention.

Even if deletion of one or more amino acids from the N-terminus of a protein results in modification of loss of one or more biological functions of the protein, other functional activities (e.g., biological activities, ability to multimerize, ability to bind a ligand) may still be retained. For example, the ability of shortened muteins to induce and/or bind to antibodies which recognize the complete or mature forms of the polypeptides generally will be retained when less than the majority of the residues of the complete or mature polypeptide are

removed from the N-terminus. Whether a particular polypeptide lacking N-terminal residues of a complete polypeptide retains such immunologic activities can readily be determined by routine methods described herein and otherwise known in the art. It is not unlikely that a mutein with a large number of deleted N-terminal amino acid residues may retain some biological or immunogenic activities. In fact, peptides composed of as few as six amino acid residues may often evoke an immune response.

Accordingly, polypeptide fragments of the invention include the secreted protein as well as the mature form. Further preferred polypeptide fragments include the secreted protein or the mature form having a continuous series of deleted residues from the amino or the carboxy terminus, or both. For example, any number of amino acids, ranging from 1-60, can be deleted from the amino terminus of either the secreted polypeptide or the mature form. Similarly, any number of amino acids, ranging from 1-30, can be deleted from the carboxy terminus of the secreted protein or mature form. Furthermore, any combination of the above amino and carboxy terminus deletions are preferred. Similarly, polynucleotides encoding these polypeptide fragments are also preferred.

The present invention further provides polypeptides having one or more residues deleted from the amino terminus of the amino acid sequence of a polypeptide disclosed herein (e.g., a polypeptide of SEQ ID NO:Y, a polypeptide encoded by the polynucleotide sequence contained in SEQ ID NO:X, and/or a polypeptide encoded by the cDNA contained in the related cDNA clone contained in a deposited library). In particular, N-terminal deletions may be described by the general formula m-q, where q is a whole integer representing the total number of amino acid residues in a polypeptide of the invention (e.g., the polypeptide disclosed in SEQ ID NO:Y), and m is defined as any integer ranging from 2 to q-6. Polynucleotides encoding these polypeptides are also encompassed by the invention.

Also as mentioned above, even if deletion of one or more amino acids from the C-terminus of a protein results in modification of loss of one or more biological functions of the protein, other functional activities (e.g., biological activities, ability to multimerize, ability to bind a ligand) may still be retained. For example the ability of the shortened mutein to induce and/or bind to antibodies which recognize the complete or mature forms of the polypeptide generally will be retained when less than the majority of the residues of the complete or mature polypeptide are removed from the C-terminus. Whether a particular polypeptide lacking C-terminal residues of a complete polypeptide retains such immunologic

activities can readily be determined by routine methods described herein and otherwise known in the art. It is not unlikely that a mutein with a large number of deleted C-terminal amino acid residues may retain some biological or immunogenic activities. In fact, peptides composed of as few as six amino acid residues may often evoke an immune response.

Accordingly, the present invention further provides polypeptides having one or more residues from the carboxy terminus of the amino acid sequence of a polypeptide disclosed herein (e.g., a polypeptide of SEQ ID NO:Y, a polypeptide encoded by the polynucleotide sequence contained in SEQ ID NO:X, and/or a polypeptide encoded by the cDNA contained in deposited cDNA clone referenced in Table 1). In particular, C-terminal deletions may be described by the general formula 1-n, where n is any whole integer ranging from 6 to q-1, and where n corresponds to the position of an amino acid residue in a polypeptide of the invention. Polynucleotides encoding these polypeptides are also encompassed by the invention.

In addition, any of the above described N- or C-terminal deletions can be combined to produce a N- and C-terminal deleted polypeptide. The invention also provides polypeptides having one or more amino acids deleted from both the amino and the carboxyl termini, which may be described generally as having residues m-n of a polypeptide encoded by SEQ ID NO:X (e.g., including, but not limited to, the preferred polypeptide disclosed as SEQ ID NO:Y), and/or the cDNA in the related cDNA clone contained in a deposited library, where n and m are integers as described above. Polynucleotides encoding these polypeptides are also encompassed by the invention.

Any polypeptide sequence contained in the polypeptide of SEQ ID NO:Y, encoded by the polynucleotide sequences set forth as SEQ ID NO:X, or encoded by the cDNA in the related cDNA clone contained in a deposited library may be analyzed to determine certain preferred regions of the polypeptide. For example, the amino acid sequence of a polypeptide encoded by a polynucleotide sequence of SEQ ID NO:X, or the cDNA in a deposited cDNA clone may be analyzed using the default parameters of the DNASTAR computer algorithm (DNASTAR, Inc., 1228 S. Park St., Madison, WI 53715 USA; http://www.dnastar.com/).

Polypeptide regions that may be routinely obtained using the DNASTAR computer algorithm include, but are not limited to, Garnier-Robson alpha-regions, beta-regions, turn-regions, and coil-regions, Chou-Fasman alpha-regions, beta-regions, and turn-regions, Kyte-Doolittle hydrophilic regions and hydrophobic regions, Eisenberg alpha- and

beta-amphipathic regions, Karplus-Schulz flexible regions, Emini surface-forming regions and Jameson-Wolf regions of high antigenic index. Among highly preferred polynucleotides of the invention in this regard are those that encode polypeptides comprising regions that combine several structural features, such as several (e.g., 1, 2, 3 or 4) of the features set out above.

Additionally, Kyte-Doolittle hydrophilic regions and hydrophobic regions, Emini surface-forming regions, and Jameson-Wolf regions of high antigenic index (i.e., containing four or more contiguous amino acids having an antigenic index of greater than or equal to 1.5, as identified using the default parameters of the Jameson-Wolf program) can routinely be used to determine polypeptide regions that exhibit a high degree of potential for antigenicity. Regions of high antigenicity are determined from data by DNASTAR analysis by choosing values which represent regions of the polypeptide which are likely to be exposed on the surface of the polypeptide in an environment in which antigen recognition may occur in the process of initiation of an immune response.

Preferred polypeptide fragments of the invention are fragments comprising, or alternatively consisting of, an amino acid sequence that displays a functional activity of the polypeptide sequence of which the amino acid sequence is a fragment.

By a polypeptide demonstrating a "functional activity" is meant, a polypeptide capable of displaying one or more known functional activities associated with a full-length (complete) protein of the invention. Such functional activities include, but are not limited to, biological activity, antigenicity [ability to bind (or compete with a polypeptide for binding) to an anti-polypeptide antibody], immunogenicity (ability to generate antibody which binds to a specific polypeptide of the invention), ability to form multimers with polypeptides of the invention, and ability to bind to a receptor or ligand for a polypeptide.

Other preferred polypeptide fragments are biologically active fragments. Biologically active fragments are those exhibiting activity similar, but not necessarily identical, to an activity of the polypeptide of the present invention. The biological activity of the fragments may include an improved desired activity, or a decreased undesirable activity.

In preferred embodiments, polypeptides of the invention comprise, or alternatively consist of, one, two, three, four, five or more of the antigenic fragments of the polypeptide of SEQ ID NO:Y, or portions thereof. Polynucleotides encoding these polypeptides are also encompassed by the invention.

Table 4.

Sequence/ Contig ID	Epitope
507291	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 843 as residues: Pro-12 to Pro-20, Lys-27 to Gly-34. Pro-67 to Arg-72, Asp-102 to Thr-111, Asp-136 to Gly-142, Ser-153 to Pro-158.
508000	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 844 as residues: Ala-16 to Trp-35.
518325	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 845 as residues: Glu-60 to Asp-67.
523111	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 846 as residues: Ser-1 to Gln-10.
532211	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 848 as residues: Cys-17 to Arg-22.
532247	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 849 as residues: Val-4 to His-10.
537932	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 850 as residues: Ser-62 to Gly-68.
540117	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 851 as residues: Pro-24 to Arg-30, Met-101 to Phe-106, Thr-138 to Asn-153.
547710	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 852 as residues: Asp-1 to Arg-7, Glu-25 to His-31, Ile-51 to Lys-56, Pro-61 to Pro-67, Gly-113 to Thr-119, Lys-125 to Asp-130, His-335 to Gly-340, Arg-364 to Pro-371.
551747	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 853 as residues: Lys-79 to Ala-88, Ser-109 to Leu-125, Asp-155 to Lys-163, Tyr-211 to Thr-219. Pro-221 to Ala-226.
552799	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 854 as residues: Gln-81 to Thr-114. Gln-200 to Arg-206.
553243	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 855 as residues: Ala-43 to Asp-48, Asp-64 to Lys-69, His-88 to Thr-94, Ala-107 to Phe-113, Leu-117 to Ser-125, Thr-132 to Glu-138, Ser-169 to Trp-181, Ser-194 to Thr-200.
553368	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 856 as residues: Ser-52 to Arg-57, Leu-76 to Gly-82, Ser-91 to Glu-96, Tyr-132 to Ala-147.
554349	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 857 as residues: Ala-31 to Gly-36, Ala-68 to Tyr-75, Gln-121 to Asp-127.
558491	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 858 as residues: Pro-1 to Arg-10.
558983	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 859 as residues: Pro-37 to Gly-42, Val-67 to Lys-84, Gln-122 to Gly-127.
589390	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 862 as residues: Glu-14 to Asn-19, Arg-68 to Ser-74, Ser-79 to Ala-84, Lys-95 to Ile-101, Lys-125 to Glu-138.
596882	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 863 as residues: Lys-15 to Lys-23, Pro-29 to Gly-34.
616289	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 864 as residues: Leu-1 to Pro-13, Thr-64 to Gly-70, Lys-119 to Arg-130.
622140	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 865 as residues: Ser-1 to Lys-6, Pro-16 to Ser-23, Arg-49 to Glu-58.
647714	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 867 as residues: Arg-1 to Gly-9, Glu-27 to Gly-36, Pro-72 to Phe-86, Pro-104 to Cys-111, Gln-145 to Lys-162, Arg-226 to Trp-233.
652156	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 871 as residues: Asn-30 to Ile-43, Ile-76 to Lys-81.
653010	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 872 as

	residues: Ser-1 to Ala-10.
655904	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 873 as residues: Ala-21 to Cys-27, Ser-76 to Gly-87, Ser-112 to Trp-121, Trp-128 to Asn-133, Glu-225 to Cys-231, Tyr-238 to Cys-248, Lys-269 to Asp-279, Phe-292 to Thr-298, Cys-357 to Ala-362, Pro-383 to Pro-388, Lys-412 to Lys-420.
657852	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 874 as residues: Arg-10 to Lys-22, Gln-48 to Glu-53, Arg-73 to Asn-86.
666414	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 875 as residues: Asn-9 to Lys-19, Arg-27 to Gly-32, Ser-58 to Thr-70, Ala-81 to Pro-86.
670188	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 877 as residues: Asn-68 to Ser-75.
670279	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 878 as residues: Lys-86 to Lys-91, Glu-101 to Val-120, Ala-130 to Glu-136.
670729	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 879 as residues: Ala-116 to Asp-134.
676496	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 881 as residues: Ile-1 to Arg-8.
678248	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 883 as residues: Ala-16 to Lys-22, Tyr-30 to Asn-35, Asp-61 to Val-70, Arg-129 to Asn-135, Thr-142 to Gly-148.
683668	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 884 as residues: Ser-3 to Gly-28, Gly-46 to Pro-56, Gly-70 to Ile-92, Gln-102 to Ser-117, Ala-123 to Pro-129, Pro-135 to Leu-140, Pro-150 to Asp-158, Pro-165 to Pro-177, Gln-188 to Asp-205, Ile-230 to Arg-245, His-251 to Trp-260, Asp-262 to Cys-267, Asn-296 to Arg-307, Glu-322 to Pro-330, Ile-351 to Asn-357, Asp-363 to Leu-369, Glu-386 to Phe-391, Lys-415 to Ser-420.
693172	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 885 as residues: Arg-11 to Arg-18, Pro-51 to Lys-58.
694303	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 886 as residues: Pro-12 to Ser-17, Leu-30 to Cys-39, Val-49 to Pro-54, Pro-67 to Leu-73, Pro-84 to Gln-90, His-99 to Leu-109.
695042	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 887 as residues: Ser-4 to Trp-28, Pro-51 to Leu-56, Asn-64 to His-70.
699799	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 888 as residues: Gln-17 to Phe-25, Glu-42 to Tyr-48, Val-52 to Gly-57, Pro-67 to Ser-73, Thr-97 to Gln-106, Gln-113 to Leu-123, Arg-171 to Asp-178, Arg-184 to Leu-191, Ile-195 to Phe-203, Lys-212 to Glu-217, Ala-236 to Asp-244, Arg-255 to Leu-260, Lys-266 to His-273, Glu-357 to Glu-363.
703015	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 890 as residues: Pro-27 to Asp-37, Gly-55 to Pro-61, His-96 to Ala-101, Glu-151 to Asn-156, Tyr-166 to Cys-178.
706391	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 891 as residues: Pro-22 to Ala-34, Pro-40 to Glu-52.
706924	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 893 as residues: Gly-1 to Gly-9, Gln-21 to Met-27.
707642	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 894 as residues: Glu-33 to Lys-40, Asn-55 to Lys-64, Tyr-104 to Cys-110, Ser-138 to Arg-148, Arg-157 to Gly-163, Lys-165 to Asn-172.
710369	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 895 as residues: Asn-1 to Thr-10.
718826	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 896 as residues: Ser-57 to Pro-63, Lys-93 to Ser-99.
719790	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 897 as residues: Phe-4 to Gln-23, Glu-47 to Ala-56, Asn-95 to Gln-102, Gln-109 to Glu-115, Arg-168 to Glu-175, Thr-196 to Arg-201, Lys-209 to Asp-215, Val-236 to Val-243.
720222	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 898 as

	residues: Glu-37 to Arg-43, Gly-62 to Pro-67. Gly-95 to Val-101, Gln-109 to Asp-114, Ala-137 to Phe-145, Asp-181 to Ser-188.
724033	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 899 as residues: Glu-55 to Glu-60, Asp-76 to Ser-85, Lys-106 to Asp-111, Gln-131 to Arg-137, Ala-172 to Gly-218.
724767	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 900 as residues: Leu-49 to Tyr-56, Tyr-114 to Glu-136, Arg-142 to Gly-148.
727065	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 901 as residues: Asn-41 to Gly-46, Lys-82 to His-88, Glu-107 to His-112, Leu-127 to Asp-132, Phe-163 to Phe-175, Thr-202 to Ile-209, Lys-229 to Gly-237, Ala-239 to Tyr-245.
727246	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 902 as residues: Pro-2 to Gly-10.
739448	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 908 as residues: His-2 to Leu-8, Gln-33 to Glu-40, Ala-44 to Glu-55, Gly-57 to Ser-67, Glu-70 to Ala-84, Glu-95 to Lys-111, Ile-186 to Asp-205, Leu-232 to Asp-238.
740060	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 910 as residues: Pro-44 to Thr-50, Arg-72 to Lys-80, Tyr-241 to Asn-251, Lys-273 to Gly-282, Ser-302 to Asn-312, Pro-337 to Ser-343, Ile-367 to Asp-376, Gly-395 to Tyr-417, Ser-442 to Gln-448.
741560	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 911 as residues: Gln-33 to Tyr-39, Pro-42 to Phe-47.
742543	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 912 as residues: Phe-10 to Tyr-15, Glu-139 to Asp-144, Glu-166 to Asn-171, Lys-175 to Glu-181.
742831	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 913 as residues: Val-64 to Glu-69.
745327	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 914 as residues: Arg-1 to Pro-13, Pro-54 to Ala-61.
745695	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 915 as residues: Trp-130 to Ser-135, Leu-199 to Thr-210, Ser-221 to Gln-229, Ala-249 to Tyr-255, Pro-257 to Pro-267, Ser-309 to Arg-314.
750316	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 916 as residues: Pro-18 to Asn-24, Thr-65 to Asp-70.
750522	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 917 as residues: Gln-10 to Lys-15.
750583	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 918 as residues: Lys-9 to Thr-15, Gln-32 to Gln-40.
751020	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 919 as residues: Arg-39 to Leu-47, Ser-107 to Ile-117, Pro-135 to Gln-144.
752196	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 920 as residues: Lys-20 to Lys-28.
753084	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 921 as residues: Lys-84 to Thr-98, Arg-128 to Ser-134, Arg-244 to Asn-252, Lys-365 to His-372.
754957	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 922 as residues: Pro-101 to Glu-106, Glu-116 to Asp-127, Ser-199 to Ile-210, Asp-217 to Asp-229, Ser-239 to Gly-244, Gln-262 to Asn-273, Pro-279 to Ser-284, Lys-318 to Arg-326, Lys-334 to Ile-341.
756557	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 923 as residues: Val-13 to Phe-21, Ile-55 to Pro-63, Ser-69 to Leu-74, Arg-82 to Leu-96, Asn-131 to Leu-139, Ile-156 to Thr-164, Thr-241 to Leu-249, Gly-273 to Ser-279, Thr-282 to Arg-289.
756712	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 924 as residues: Ile-4 to Thr-37, Gln-42 to Ser-48, Asn-56 to Lys-69, Ser-79 to Ser-85.
757414	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 925 as residues: Glu-14 to Thr-23, His-50 to Arg-62, Tyr-72 to Cys-78, Gly-121 to Pro-128.

757614	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 926 as residues: Gly-13 to Cys-19, Thr-32 to Glu-38, Val-44 to Gln-53, Lys-55 to Asp-60, Gln-65 to Glu-70, Lys-89 to Glu-105, Glu-112 to Asp-142, Glu-147 to Arg-152, Glu-211 to Leu-216, Leu-227 to Ser-232, Lys-245 to Lys-255, Glu-278 to Tyr-291, Gln-297 to Arg-303.
759878	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 928 as residues: Trp-16 to Glu-21, Trp-45 to Pro-54, Ile-154 to Phe-162, Gly-174 to Leu-181.
760227	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 929 as residues: Arg-99 to Asp-104.
766051	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 931 as residues: Asp-10 to Lys-19.
768053	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 933 as residues: Ile-1 to Tyr-7, Phe-52 to Cys-61, Val-118 to Ser-125.
768055	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 934 as residues: Asp-39 to Ser-46, Lys-92 to Lys-99, Val-165 to Phe-172, Lys-252 to Ala-261, Asn-268 to Ala-273.
769685	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 935 as residues: Pro-129 to Arg-135.
771920	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 936 as residues: Pro-47 to Val-53, Asp-85 to Phe-97, Val-136 to Gly-144, Pro-166 to Glu-172, Leu-190 to Ser-197.
772790	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 937 as residues: Leu-5 to Trp-13, Met-20 to Leu-39, Ile-50 to Pro-63, Glu-66 to Ser-72, Leu-112 to Gln-120, Ala-141 to Lys-146, Tyr-165 to Asp-173.
772916	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 938 as residues: Lys-16 to Arg-25.
773632	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 940 as residues: Arg-1 to His-33.
774364	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 941 as residues: Ser-97 to Asn-103.
775355	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 942 as residues: Ser-40 to Ala-46.
775844	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 943 as residues: Leu-20 to Ser-31, Thr-38 to Val-47.
777760	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 944 as residues: Thr-22 to Ser-28, Thr-35 to Glu-42, Met-47 to Thr-55.
779837	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 945 as residues: Thr-26 to Arg-31, Leu-75 to Lys-100.
780769	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 946 as residues: Gly-1 to Asp-7, Lys-25 to Lys-31, Tyr-65 to Gly-70, Thr-100 to Arg-106, Pro-118 to Glu-124, Lys-162 to Ser-172, Leu-176 to Leu-182.
781445	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 947 as residues: Asn-33 to Lys-38, Leu-67 to Met-73, Ser-111 to Lys-121, Lys-127 to Leu-134, Pro-153 to Trp-158, Lys-237 to Met-249, Pro-280 to Tyr-292.
781531	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 948 as residues: Ala-8 to Pro-23, Gln-56 to Cys-61, Asn-66 to Pro-72.
783018	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 949 as residues: Asn-4 to Leu-17, Gly-19 to Phe-26, Pro-37 to Glu-43, Val-58 to Ser-64, Gln-80 to Gly-85.
783097	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 950 as residues: Pro-1 to Asp-9, Pro-24 to Gly-40, Pro-47 to Thr-55, Gln-62 to Ser-76.
784198	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 951 as residues: Met-1 to Arg-15, Leu-43 to Glu-48, Asp-55 to Asp-62, Ser-111 to Lys-160.
784868	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 952 as residues: Trp-8 to Gly-17, Glu-20 to Arg-35, Gly-40 to Cys-45, Ser-59 to Ser-64, Ala-73 to Leu-78, Val-85 to Leu-91, Arg-130 to Lys-135, Leu-138 to Glu-146, Pro-188 to

	Pro-194, Ser-206 to Cys-212, Ser-232 to Ala-246, Asp-293 to Ser-298.
785428	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 953 as residues: Arg-9 to Met-20, Glu-28 to Gly-33, Asn-49 to Lys-57, Thr-67 to Arg-75, Ser-81 to Leu-87, Glu-103 to Thr-109, Pro-115 to Ile-120, Asn-146 to Ser-174, Ser-177 to His-195, Met-197 to Ile-221, Asp-232 to Glu-240, Glu-289 to Phe-302, Cys-306 to Arg-314, Ser-357 to Ser-366, Lys-385 to Glu-401, Val-419 to Asp-427.
785845	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 954 as residues: Arg-41 to Asp-52, Pro-82 to Arg-94, Pro-102 to Gln-107, Gln-170 to Tyr-181, Glu-248 to Lys-254, Asp-277 to Gly-287, Ala-302 to Arg-308, Thr-367 to Gly-374.
785854	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 955 as residues: Asp-1 to Asp-17, Cys-59 to Asp-65.
787279	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 958 as residues: Lys-13 to Lys-20.
789002	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 959 as residues: Met-20 to Glu-29.
789008	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 960 as residues: Ser-24 to Arg-33, Ile-44 to Gly-57, Arg-63 to Asn-72, Ile-76 to Pro-82.
789555	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 961 as residues: Trp-106 to Thr-117, Trp-156 to Gln-163, Gln-173 to Asp-178, Gln-227 to Glu-233, Gln-255 to Glu-261, Glu-297 to Tyr-306, Thr-339 to Val-345, Leu-378 to Ile-385, Asp-414 to Lys-420, Cys-437 to Ile-444, Thr-491 to Gln-497, Glu-509 to Ser-515, Lys-526 to Glu-538.
789631	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 962 as residues: Thr-10 to Gly-18.
789779	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 963 as residues: Glu-1 to Ala-13, Leu-103 to Ser-109.
790387	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 964 as residues: His-1 to Ala-12.
790461	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 965 as residues: Glu-14 to Gly-23, Asp-47 to Met-53, Ala-55 to Thr-60, Pro-67 to Thr-73, Pro-78 to Gly-86, Tyr-91 to Pro-101, Ala-133 to Asn-139, Glu-169 to Gln-182, Glu-189 to Thr-195, Asn-197 to Arg-203, Gln-265 to Asp-271.
790931	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 966 as residues: Val-3 to Glu-13, Pro-29 to Pro-35, Glu-116 to Arg-125.
791176	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 967 as residues: Pro-1 to Pro-10, Pro-17 to Phe-28, Ser-61 to Pro-67.
792539	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 969 as residues: Ser-12 to Trp-17, Gln-20 to Lys-29, Asp-45 to Glu-51, Tyr-75 to Lys-83, Arg-103 to Gly-119, Gln-145 to Lys-155, Lys-166 to Leu-180, Thr-195 to Gly-203, Gln-209 to Val-219, Ser-222 to Ala-244, Leu-251 to Leu-260, Lys-277 to Lys-285.
792749	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 970 as residues: Ala-22 to Asp-41, Thr-61 to Met-66, Asp-191 to Lys-198, Arg-280 to Phe-287, Thr-289 to Lys-299, Pro-325 to Asp-332, Ser-351 to Arg-357.
793206	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 972 as residues: Gly-1 to Arg-6, Gln-11 to Arg-22, Glu-86 to Asp-91.
793626	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 974 as residues: Ser-1 to Gly-13, Gly-17 to Asn-26.
794417	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 975 as residues: Ser-7 to Trp-16.
795197	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 976 as residues: Ser-67 to Glu-73, Arg-129 to Gly-136, Phe-154 to Ala-161, Tyr-198 to Tyr-203, Pro-206 to Asp-212, Glu-222 to Cys-231.
795251	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 977 as residues: Phe-44 to Ser-50, Asp-57 to Pro-62, Asn-80 to His-90, Ser-110 to Ala-115, Ile-141 to Val-148, Glu-155 to Thr-173, Val-202 to Pro-217, Ile-221 to Val-229, Thr-

	233 to Ser-243, Val-253 to Thr-259, Ala-290 to Asn-320, Pro-322 to Ile-330, Ala-333 to Met-344, Val-362 to Leu-367, Asp-397 to Val-402, Glu-422 to Gly-448, Met-453 to Gly-460.
795752	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 978 as residues: Pro-52 to Asn-63, Pro-70 to Ile-79, Arg-93 to Gln-111.
796261	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 979 as residues: His-1 to Val-6, Cys-10 to Ser-15, Gly-26 to Ser-34, Trp-36 to Pro-58, Pro-96 to Thr-102, Pro-111 to Tyr-116, Phe-131 to Gly-138, Pro-184 to Leu-190, Glu-237 to Gly-244, Pro-255 to Lys-267, Lys-271 to Leu-280.
796933	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 980 as residues: Arg-1 to Pro-14, Gln-47 to Cys-52, Asn-57 to Pro-63, Ser-277 to Lys-282.
799424	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 981 as residues: Tyr-18 to Leu-27, Met-50 to Met-60, Leu-169 to His-178, Ser-233 to Ser-241.
799698	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 982 as residues: Pro-16 to Pro-21, Ala-54 to Glu-61, Ala-96 to Gly-105.
800351	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 983 as residues: Gly-21 to Gln-34, His-39 to Lys-53, Ser-63 to Tyr-71.
800573	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 984 as residues: Asp-33 to Arg-39, Ala-43 to Leu-48, Glu-256 to Gln-266, Gly-305 to Ile-311, Pro-314 to Ala-320, Gln-388 to Asn-394.
805815	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 985 as residues: Arg-1 to Lys-22, Ser-34 to Arg-48, Thr-64 to Arg-70, Pro-81 to Phe-89, Arg-148 to Asn-154, Tyr-172 to Asp-185, Ser-205 to Asp-216, Tyr-278 to His-285, His-294 to Pro-299, Glu-326 to Gly-333, Gly-336 to Ser-345.
806445	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 986 as residues: Arg-15 to Gly-24, Lys-26 to Trp-32.
810309	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 987 as residues: Pro-33 to Phe-50, Ile-57 to Gly-62, Gln-72 to Asn-85, Ala-87 to Thr-172.
811022	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 988 as residues: Ala-1 to Met-11, Gln-62 to Trp-68, Ala-89 to Val-99.
811023	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 989 as residues: Tyr-54 to Lys-61, Met-64 to Thr-70.
811143	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 990 as residues: Ala-1 to Ser-7, Ser-19 to Gly-36, Arg-53 to Pro-58, Thr-87 to Glu-102, Arg-115 to Tyr-120, Thr-159 to Thr-164, Ala-171 to Ser-179, Ala-206 to Pro-217, Pro-224 to Ala-233, Arg-253 to Ser-259.
813000	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 993 as residues: Tyr-25 to Lys-30, Lys-36 to Ile-43, Lys-52 to Gln-69, Glu-76 to Asp-81, Arg-92 to Trp-104, Leu-120 to Lys-126, Ser-129 to Ser-135, Ser-139 to Thr-156, Pro-165 to Glu-178, Ser-181 to Thr-186, Tyr-196 to Lys-201, Cys-225 to Lys-230, Glu-234 to Ser-242.
813431	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 995 as residues: Leu-23 to His-29, Pro-38 to Leu-46, Ser-59 to Gly-68, Pro-85 to Lys-108, Arg-119 to Phe-124, Ser-139 to Lys-156.
813450	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 996 as residues: Asn-1 to Trp-10.
813478	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 997 as residues: Ala-8 to Arg-14, Ile-64 to Thr-69, Val-94 to Asp-101, His-112 to Gln-117, Tyr-139 to Glu-145, Tyr-195 to Cys-208, Gly-216 to Gly-223, Asp-297 to Ser-307, Gly-378 to Leu-383, Ile-391 to Pro-404, Asn-451 to Ser-466.
813505	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 998 as residues: Thr-1 to Ala-20, Pro-22 to Lys-27, His-44 to Thr-51, Pro-53 to Thr-60, Arg-62 to Lys-79, Lys-97 to Asn-103, Pro-139 to Lys-144.
815552	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 999 as residues: Pro-1 to Ser-6, Pro-25 to Cys-31, Arg-142 to Lys-150.

815606	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1000 as residues: Arg-1 to Ala-11.
816048	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1001 as residues: Ala-13 to Thr-24, Glu-30 to Gln-39, Arg-69 to Gly-77, Gln-119 to Gly-126, Tyr-156 to Asn-162, Ser-184 to Gly-191.
823981	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1004 as residues: Lys-1 to Cys-7, Ala-11 to Lys-17, Glu-90 to Ile-95, Asn-141 to Arg-148, Leu-158 to Ala-163, Ala-171 to Thr-177.
824364	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1005 as residues: Gln-43 to Gly-54.
824423	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1006 as residues: Cys-33 to Arg-42, Val-53 to Met-63, Lys-71 to Lys-78, Gly-107 to Pro-118, Ala-159 to Leu-165, Val-272 to Arg-284, Pro-422 to Pro-427, Arg-437 to Gln-443, Ala-474 to Asp-482, His-519 to Cys-525, Ala-529 to Gln-535, Arg-540 to Gln-548.
825279	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1007 as residues: Ser-8 to Arg-14, Asp-23 to Gly-28, Ser-30 to Pro-37, His-52 to Ala-57, Pro-65 to Ser-74. Pro-112 to Ser-118, Ala-181 to Pro-189.
825548	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1009 as residues: Pro-2 to Ser-9.
825725	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1010 as residues: Pro-1 to Gly-8, Leu-95 to Lys-100, Glu-118 to Thr-125, Ser-162 to Lys-167, Arg-201 to Tyr-206.
827079	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1012 as residues: Arg-9 to Ser-17.
827153	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1013 as residues: Val-32 to Ala-44, Pro-49 to Ser-57, Gln-77 to Gly-82, Asp-116 to Gly-127, Arg-165 to Asn-172.
827351	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1014 as residues: Gly-5 to Lys-11, Ser-59 to Lys-67, Glu-130 to Arg-136, Asn-176 to Leu-183.
827503	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1015 as residues: Asp-61 to Val-67, Arg-113 to Asp-119, Ser-180 to Gly-191, Pro-199 to Ser-211, Ser-228 to Asn-238, Gly-276 to Ser-286, His-343 to Gly-351, Gln-354 to Arg-366, Leu-368 to Gln-382, Pro-393 to Ser-400, Asp-412 to Cys-418, Gly-430 to Leu-435, Gln-445 to Asp-450, Lys-484 to Val-491, Leu-513 to Gly-520.
827563	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1016 as residues: Pro-69 to Ala-81, Pro-84 to Gly-91, Ala-106 to Leu-112, Arg-216 to Lys-224, Trp-239 to Gly-250.
827565	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1017 as residues: Ala-1 to Ser-8, Ser-88 to Gly-96, Asn-121 to Asp-128, Cys-191 to Gly-196, Met-242 to Thr-248.
827893	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1018 as residues: Ser-41 to Ala-50, Glu-72 to His-77, Ala-120 to Glu-125, Thr-144 to Ile-153.
828072	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1019 as residues: Lys-30 to Leu-35.
828241	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1021 as residues: Gly-35 to Phe-45, Pro-47 to Arg-55, Glu-62 to Leu-70, Arg-102 to Tyr-111, Phe-128 to Gln-134, Val-139 to Met-144, Ser-180 to Gly-188, Lys-214 to Leu-219, Ser-241 to Glu-246, Phe-292 to Thr-298.
828287	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1022 as residues: Ala-12 to Thr-21, Ala-23 to Gly-31, Leu-43 to Gly-51, Lys-127 to Val-134.
828371	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1024 as residues: Gln-1 to Ala-6, Lys-50 to Pro-71, Pro-98 to Ser-111, Asp-148 to His-164, Asp-185 to Arg-191, Asp-238 to Gly-244, Pro-262 to Cys-274.
828403	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1025 as residues: Gly-1 to Trp-15, Arg-73 to Leu-82.
828501	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1026 as

	residues: Arg-99 to Arg-105, Pro-171 to Ser-176, Lys-189 to Val-195, Lys-291 to Ala-296.
828527	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1028 as residues: Glu-58 to Cys-63.
828538	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1029 as residues: Pro-9 to Thr-24, Thr-46 to Gly-52, Ser-70 to Thr-76, Ser-142 to Thr-149, Pro-154 to Ser-171, Glu-189 to Ser-196.
828541	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1030 as residues: Arg-9 to Pro-23, Gln-64 to Leu-69, Asp-76 to Asn-83, Lys-88 to Gln-93, Pro-129 to Thr-135, Gly-194 to Gly-203, Asp-223 to Gly-231, Thr-265 to Ile-281, Leu-287 to Lys-297.
828549	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1031 as residues: Pro-22 to Asn-28.
828562	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1032 as residues: Arg-26 to Asp-33, Asp-42 to Pro-58, Thr-63 to Lys-70, Thr-103 to Asp-114.
828576	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1033 as residues: Arg-11 to Gly-17, Pro-26 to Gly-31, Ala-48 to His-58.
828602	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1034 as residues: Tyr-1 to Met-8, Leu-10 to Lys-26, Pro-47 to Pro-54, Lys-128 to Ser-133.
828628	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1035 as residues: Thr-124 to Thr-129, Gly-136 to Phe-142, Asp-164 to His-171, Asp-180 to Tyr-194.
828684	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1037 as residues: Ser-16 to Thr-22, Arg-39 to Ala-51, Arg-60 to Gly-65, Thr-67 to Arg-90, Lys-109 to Gln-125, Ser-146 to Arg-159, Gln-166 to Thr-176, Glu-192 to Tyr-197, Val-267 to His-279, Ala-351 to Gly-356, Phe-363 to Gly-368, Gly-387 to Arg-392, Asp-488 to Ala-498.
828727	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1038 as residues: Gly-14 to Val-21, Asp-40 to Gln-57, Gln-86 to Tyr-93, Gln-98 to Asp-104, Lys-124 to Asp-130, Gln-138 to Cys-156, Tyr-170 to Gln-175, Gln-196 to Ala-201.
828734	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1039 as residues: Asp-5 to Trp-19, Ile-37 to Pro-42, Asp-52 to Asp-72, Glu-85 to Ser-92, Ser-107 to Leu-117, Asp-128 to His-147.
828842	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1041 as residues: Ala-25 to Phe-32, Glu-54 to Ser-61, Thr-74 to Glu-79, Glu-99 to Lys-105, Glu-112 to Glu-121.
828843	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1042 as residues: Pro-3 to Asn-11, Gln-46 to Ala-51, Asn-62 to Lys-74, Val-108 to Gln-113, Arg-119 to Gly-163, Ala-223 to Lys-237.
828851	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1043 as residues: Thr-3 to Lys-8, Leu-63 to Val-70, Lys-141 to Val-149, Ile-326 to Thr-333.
828856	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1044 as residues: Leu-1 to Gly-10.
828862	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1045 as residues: Pro-1 to Pro-9, Arg-81 to Glu-87, Gln-114 to Glu-119.
828870	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1046 as residues: Ser-1 to Gly-18, Trp-25 to Gly-31, Arg-46 to Ser-52, Ala-103 to Ala-108, Ser-154 to Gly-165, Gln-228 to Pro-236, Ser-284 to Gly-291, Ala-321 to Asp-327, Lys-377 to Asn-394, Asp-406 to Ser-416.
828873	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1047 as residues: Tyr-15 to Gly-20, Asn-72 to Asp-80, Pro-105 to Pro-110, Gln-149 to Arg-154, Glu-161 to Gly-167, Ile-312 to Asp-318, Lys-353 to Leu-361, Arg-379 to Thr-385, Pro-423 to Trp-435, Pro-437 to Cys-444, Asn-450 to Met-466.
828892	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1048 as residues: Asp-19 to Asn-25, Gly-67 to Glu-79.
828893	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1049 as

	residues: Ser-55 to Thr-60, Glu-97 to Ser-103, Thr-164 to Glu-170, Gly-192 to Gly-197, Leu-204 to Ser-218, Ala-238 to Ser-250, Asp-265 to Tyr-292, Gly-298 to Gly-307, Gly-351 to Met-359, Phe-389 to Glu-400.
828897	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1050 as residues: Phe-28 to Arg-33.
828910	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1051 as residues: His-1 to Ile-13, Arg-20 to Glu-64, Arg-83 to Gln-89, Tyr-145 to Asp-152.
828927	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1052 as residues: Glu-10 to Pro-21, Thr-54 to Gly-60, Cys-79 to Glu-90, Lys-154 to Lys-159.
828932	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1053 as residues: Arg-1 to Arg-9, Phe-54 to Pro-60, Gln-74 to Gly-90, Asn-114 to Gly-119, Cys-124 to Ser-132, Thr-139 to Leu-151, Asp-171 to Lys-182, Ala-188 to Leu-193, Val-203 to Trp-222, Lys-230 to Glu-236, Glu-244 to Asp-250, Leu-258 to Gly-268, Gly-283 to Asp-288, Ser-291 to Trp-297, Gly-300 to Ala-308.
828933	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1054 as residues: Glu-21 to Ser-34, Thr-130 to Tyr-138.
828941	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1055 as residues: Gly-1 to Ala-6, Pro-15 to Gly-22, Asn-160 to Gln-177, Asn-193 to Asp-199, Glu-205 to Leu-211.
828963	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1057 as residues: Pro-48 to Gly-54, Ser-56 to Ser-76, Lys-102 to Pro-107, Ser-146 to Gly-153, Ser-208 to Arg-213, Tyr-285 to Leu-299, Pro-314 to Phe-319, Asn-322 to Asn-327.
828964	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1058 as residues: Thr-36 to Cys-47.
828966	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1059 as residues: Gly-1 to Ser-16, Met-26 to Pro-31, Lys-128 to Glu-134, His-165 to Gln-170, Asp-207 to Asn-216, Pro-348 to Arg-359, Lys-433 to Ala-439, Gly-448 to Tyr-457.
828967	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1060 as residues: Met-135 to Arg-141, Gly-149 to Lys-166, Ile-188 to Ser-196, Gly-203 to Tyr-213, Gln-267 to Asp-278, Arg-298 to Trp-317, Leu-319 to Leu-326, Gln-344 to Thr-349, Pro-410 to Ser-419, Ala-500 to Ala-510.
828977	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1061 as residues: Gly-32 to Tyr-42, Asn-52 to Glu-58, Ser-78 to Gly-87, Lys-97 to Gly-109, Glu-116 to Arg-127, Pro-147 to Pro-152, Pro-162 to Asn-171, Leu-179 to Glu-185, Ile-203 to Glu-208, Val-222 to Gln-228.
828978	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1062 as residues: Asp-24 to Lys-30, Arg-49 to Lys-62, Arg-121 to Thr-149, Gly-163 to Leu-171, Ala-186 to Glu-195, Glu-216 to Ser-221, Ile-229 to Ser-236, Lys-258 to Lys-264, Lys-305 to Arg-313.
829001	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1064 as residues: Thr-11 to Cys-24, Arg-48 to His-55, Arg-62 to Gly-70.
829003	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1065 as residues: Lys-14 to Gly-22, Ser-61 to Asp-66, Cys-80 to Lys-91, Lys-97 to Arg-107, Gly-135 to Asn-146, Lys-198 to Lys-208, Met-221 to Thr-227, Phe-244 to Gly-256, Asp-292 to Gln-300.
829016	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1066 as residues: Arg-1 to Asp-11, Ala-17 to Gln-25, Glu-30 to His-37, Cys-39 to Thr-44, Asn-86 to Phe-93.
829027	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1067 as residues: Pro-1 to Ser-7, Thr-45 to Leu-63, Arg-113 to Thr-118, Pro-172 to Gly-182.
829028	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1068 as residues: Ser-1 to Gln-19, Gly-32 to Phe-39, Ala-95 to Arg-116, Lys-122 to Glu-142, Ile-148 to Asn-156, Ser-168 to Asn-191, Ala-196 to Thr-204, Ser-289 to Lys-304, Leu-308 to Ser-314, Thr-332 to Ile-341.
829034	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1070 as residues: Ser-32 to Ala-43, Thr-62 to Glu-69, Phe-128 to Thr-156, Thr-179 to His-188,

	Gly-196 to Glu-203. Pro-205 to Ala-219, Gln-221 to Ile-230, Pro-246 to Thr-255, Thr-271 to His-276, Asn-324 to Thr-344, Pro-364 to Ala-370, Tyr-427 to Arg-434, Gly-440 to Pro-445.
829036	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1071 as residues: Leu-16 to Phe-21, Thr-69 to Lys-74, Asn-87 to His-92, Thr-126 to Leu-137, Phe-154 to Lys-164, Ala-171 to Asp-178, Ile-192 to Thr-203, Glu-261 to Ser-273.
829049	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1072 as residues: Gly-50 to Tyr-59.
829073	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1073 as residues: Asn-1 to Met-6, Asn-26 to Ser-35, Pro-43 to Ile-54.
829075	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1074 as residues: Gly-14 to Pro-30, Ser-64 to Ser-69, Asn-97 to Arg-109.
829076	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1075 as residues: Lys-84 to Gly-94, Asn-142 to Ile-147.
829080	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1076 as residues: Gly-13 to Trp-23, Pro-39 to Gly-44.
829087	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1077 as residues: Pro-13 to Arg-24.
829095	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1079 as residues: Pro-8 to Pro-13.
829118	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1081 as residues: Arg-7 to Val-12, Ile-52 to Thr-70, Ser-86 to Asp-91, Thr-126 to Ser-138.
829152	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1082 as residues: Asp-12 to Ser-19.
829160	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1083 as residues: Ala-7 to Arg-20.
829163	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1084 as residues: Ser-23 to Asp-32, Val-36 to Glu-59, Ser-65 to Asn-76, Cys-91 to Ser-102, Pro-108 to Leu-115, Thr-151 to Gln-164, Glu-167 to Lys-176.
829176	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1085 as residues: His-1 to Asn-8, Cys-22 to Arg-27, Gly-34 to Ser-44, Tyr-60 to Ser-65, Ser-118 to Gln-123, Ser-149 to Trp-154, Pro-159 to Gly-168, Gln-207 to Leu-220.
829204	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1086 as residues: Ala-11 to Ser-19, Thr-104 to Lys-133.
829207	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1087 as residues: Lys-5 to Ser-11, Pro-31 to Ser-37, Pro-87 to Asp-92, Asp-115 to Lys-123, Ser-149 to Arg-155, Thr-243 to Pro-253.
829228	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1088 as residues: Pro-1 to Trp-6, Leu-73 to Tyr-79, Glu-108 to Thr-117, Asp-136 to Asp-142, Ser-201 to Pro-207, Leu-224 to Pro-233, Val-242 to Ala-248, Ser-312 to Leu-319, Val-349 to Ser-359, Ala-362 to His-368, Thr-370 to Gly-376, Lys-403 to Tyr-409, Glu-426 to Arg-431, Lys-455 to Asp-460, Arg-499 to Thr-505, Asp-561 to Ser-570, Ser-665 to Ser-673.
829252	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1089 as residues: Thr-9 to Val-16.
829269	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1091 as residues: Ser-1 to Glu-7, Lys-76 to Gln-83.
829277	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1092 as residues: Lys-88 to Phe-97, Thr-106 to Leu-120, Thr-147 to Pro-152, Pro-173 to Met-179.
829290	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1093 as residues: Pro-1 to Pro-19, Pro-25 to Lys-30.
829308	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1096 as residues: Met-26 to Asn-37, Glu-42 to Gln-51, Thr-68 to Ser-95, Ala-97 to Lys-113, Asp-156 to Val-161, Val-208 to Asp-215, Pro-217 to Ala-228.
829349	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1097 as

	residues: Asn-18 to Lys-24, Asp-87 to Asn-94, Glu-116 to Gly-125.
829354	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1098 as residues: Ala-1 to Asn-16, Pro-36 to Arg-43.
829388	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1099 as residues: Glu-91 to Pro-100, Tyr-122 to Thr-127, Thr-168 to Val-173, Thr-210 to Asp-215, Leu-219 to Gly-224, Gly-232 to Val-237.
829626	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1101 as residues: Gly-145 to Ala-151.
829730	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1102 as residues: Pro-22 to His-27, Pro-87 to Asp-93, Arg-109 to Lys-115, Arg-172 to Glu-177, Glu-219 to Asp-226.
829892	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1103 as residues: Tyr-36 to Ala-46, Val-58 to Asn-63, Glu-73 to Asn-78, Asn-90 to Asn-95, Ser-125 to Leu-133, Glu-143 to Pro-150, Phe-186 to Leu-191, Leu-274 to Glu-281, Lys-303 to Phe-308, Thr-323 to Gly-330.
829938	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1105 as residues: Thr-1 to Pro-14, Ser-36 to Thr-57, Ser-81 to Thr-91, Glu-103 to Leu-110, Glu-124 to Tyr-130, Ala-135 to Lys-140, Leu-146 to Glu-162, Lys-167 to Glu-172, Glu-199 to Val-213.
829969	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1106 as residues: Arg-12 to His-21, Arg-77 to Ser-88.
829982	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1107 as residues: Arg-6 to His-14, Ser-40 to Met-47, Thr-68 to Cys-74, Ile-97 to His-115, Gly-118 to Pro-124.
830007	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1108 as residues: Ala-7 to Ala-16.
830019	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1109 as residues: Leu-21 to Pro-27.
830073	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1110 as residues: Gly-16 to Val-22, Pro-45 to Lys-50, Phe-58 to Arg-65, Ser-135 to Gly-141, Gly-153 to Ser-158, Pro-160 to Tyr-168.
830148	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1114 as residues: Asp-63 to Lys-81, Gly-101 to Gly-108, Pro-182 to Ala-200, Pro-210 to Met-216, Pro-235 to Gly-243.
830183	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1117 as residues: Pro-29 to Lys-37, Pro-40 to Val-47, Tyr-62 to His-67.
830194	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1118 as residues: Ala-43 to Lys-51, Glu-66 to Leu-74, His-81 to Glu-88, Arg-98 to Ser-105, Gly-111 to Gln-116, Leu-166 to Lys-182, Leu-261 to Ala-273, Glu-294 to Arg-302, Glu-335 to Asp-347.
830207	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1119 as residues: Pro-14 to Pro-48, Asp-55 to Gly-61, Lys-94 to Asn-99, Ala-107 to Ser-115, Ile-117 to Asn-124, Thr-133 to Cys-139, Thr-142 to Ile-147, Gly-163 to Ser-169.
830242	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1120 as residues: Glu-29 to Lys-34, Leu-151 to Gln-157, Arg-160 to Ser-171, Gln-177 to Pro-190.
830328	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1121 as residues: Pro-18 to Met-24, Glu-66 to Gln-78, Ala-85 to Arg-93, Glu-99 to His-108, Leu-114 to Asp-137, Pro-171 to Gln-176, Gly-205 to Leu-213.
830340	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1122 as residues: Gly-12 to Lys-18, Arg-46 to Glu-56, Leu-67 to Gly-73, Ala-91 to Tyr-112.
830341	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1123 as residues: Leu-14 to Gln-20, Asn-34 to Glu-41, Lys-193 to Asn-198.
830351	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1124 as residues: Pro-1 to Leu-13, Gly-42 to Pro-51, Arg-64 to Ala-69, Met-104 to Asp-109, Cys-125 to Trp-132, Asp-161 to Trp-175, Glu-206 to Glu-218.

830358	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1125 as residues: Cys-75 to Thr-81.
830400	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1127 as residues: Pro-1 to Gly-6, Arg-17 to Arg-33, Glu-151 to Trp-157, Ile-187 to Tyr-193, Lys-249 to Glu-258, Asn-289 to Ser-294, Pro-340 to Lys-353.
830437	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1128 as residues: Ala-87 to Ser-94, Asp-104 to Arg-112, Leu-114 to Asp-119, Ser-186 to Thr-202.
830466	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1130 as residues: Pro-14 to Ile-24, Thr-35 to Phe-42, Ser-45 to Asn-57, Pro-65 to Trp-89.
830497	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1131 as residues: Thr-1 to Leu-9, Ser-46 to Leu-56, Glu-117 to Lys-124, Pro-129 to Asp-135, Ala-144 to Gln-150, Gly-156 to Lys-162, Phe-182 to Pro-187, Pro-196 to Gln-201, Lys-217 to Asp-227.
830511	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1132 as residues: Lys-13 to Cys-44, Lys-101 to Arg-109, Gln-120 to Gly-129.
830540	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1135 as residues: Leu-31 to Lys-37, Arg-48 to Asn-54.
830550	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1136 as residues: Pro-8 to Cys-15, Val-80 to Cys-85.
830567	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1137 as residues: Lys-28 to Leu-33, Pro-60 to Ser-66.
830586	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1138 as residues: Pro-1 to Gln-15, Arg-33 to Leu-40, Arg-72 to Ser-78, Leu-98 to Asp-103, Phe-116 to Gly-124, Pro-152 to Arg-158, Thr-193 to Pro-200, Leu-213 to Phe-219, Asp-229 to Lys-237, Lys-246 to Lys-258, Arg-275 to Thr-280, Thr-306 to Lys-312, Leu-320 to Arg-328, Ala-335 to Asn-340, Gly-342 to Trp-349, Cys-364 to Pro-372.
830632	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1139 as residues: Ala-6 to Thr-14, Arg-143 to Lys-148.
830659	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1142 as residues: Thr-32 to Tyr-40, Ala-67 to Gln-82, Arg-128 to Thr-133, Leu-137 to Thr-146, Pro-187 to Ser-193.
830696	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1143 as residues: Glu-83 to Lys-91.
830743	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1145 as residues: Pro-11 to Phe-16, Thr-48 to Ser-60.
830770	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1146 as residues: Thr-36 to Thr-44.
830830	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1147 as residues: Lys-73 to Thr-78, Pro-84 to Pro-96, Lys-107 to Glu-124, Ile-142 to Cys-153, Asp-179 to Asn-184.
830838	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1148 as residues: Ser-17 to Arg-22, Gly-48 to Val-56, Asn-217 to Asp-223, Thr-238 to Asn-243.
830851	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1149 as residues: Arg-1 to Val-7, Ala-156 to Phe-162, Arg-216 to Lys-239.
830856	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1151 as residues: Trp-29 to Gly-35, Thr-41 to His-47, Val-95 to Lys-111.
830862	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1152 as residues: Arg-14 to Val-22, Ala-24 to Gly-35, Arg-37 to Lys-58, Ala-88 to Ala-94, Lys-164 to Ser-172.
830879	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1153 as residues: Cys-34 to Leu-44, Ser-60 to Gly-69, Asp-118 to Gly-123, Cys-148 to Gln-154.
830919	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1154 as residues: Pro-1 to Ser-41, Arg-53 to Pro-61, Arg-66 to Gln-132.

830969	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1155 as residues: His-17 to Pro-27, Phe-31 to Val-38, Gly-53 to Thr-62.
830991	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1156 as residues: Arg-1 to Pro-14, Ala-44 to Ser-56, His-69 to Lys-75, Gly-89 to Lys-98, Tyr-101 to Tyr-121, Pro-123 to Thr-131, Pro-149 to Gly-171, Tyr-186 to Glu-192.
831002	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1157 as residues: Glu-63 to Asn-73, Pro-114 to Tyr-122, Ser-194 to Glu-201, Ile-263 to Ser-269.
831003	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1158 as residues: Ile-9 to Leu-17, Asp-63 to Gly-70, Leu-112 to Ala-128.
831021	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1159 as residues: Asn-6 to Asp-12.
831036	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1160 as residues: Ser-6 to Ser-25, Tyr-37 to Lys-42, Arg-49 to Tyr-54, Pro-56 to Glu-61, Gln-72 to Cys-77, Lys-104 to Glu-110, Lys-134 to Met-142, Asp-147 to Arg-158, Arg-189 to Asn-194.
831071	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1161 as residues: Thr-41 to Arg-49, Glu-137 to Asp-142, Tyr-158 to Glu-163, Arg-184 to Thr-199, Arg-239 to Gly-253, Pro-297 to Gly-304, Pro-319 to Ile-327, Leu-347 to Val-356, Asn-435 to Leu-441, Asp-443 to Ser-452, Ala-457 to Thr-462, Asp-479 to Arg-484, Gly-510 to His-516, Glu-555 to Thr-565, Asp-597 to Ser-602, Thr-615 to Asp-622, Val-653 to Leu-661, Ala-684 to Arg-697, Ser-704 to Glu-712, Ala-731 to Ala-737, Lys-800 to Met-805.
831099	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1163 as residues: Leu-12 to Gly-18, Leu-93 to Ile-98, Lys-165 to Ser-183, Thr-198 to Lys-211, Glu-232 to Gly-237, Pro-239 to Gly-249, Arg-257 to Asp-278, Cys-292 to Glu-297, Arg-306 to Ser-316, Asp-323 to Asn-331, Glu-347 to Gly-354, Thr-365 to Asn-370, Pro-390 to Thr-396, Asn-420 to Ser-433, Val-440 to Gln-451, His-457 to Asp-465, Phe-533 to Met-538, Ala-540 to Tyr-550, Pro-560 to Lys-565.
831113	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1164 as residues: Ser-26 to Arg-33, Pro-51 to Thr-56, Cys-82 to Asp-94, Pro-104 to Gly-128.
831120	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1165 as residues: Ala-39 to Leu-47, Val-49 to Lys-55, Thr-66 to Asp-75, Thr-85 to Gly-104, Ala-114 to Gly-147, Pro-176 to Thr-199, Ser-205 to Ser-221, Glu-233 to Lys-240, Lys-246 to Asp-251, Glu-256 to Ser-267, Ser-291 to Leu-302, Thr-305 to Asp-324, Cys-336 to Val-345, Phe-367 to Cys-375.
831172	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1166 as residues: Pro-1 to Gly-7, His-119 to Gly-125, His-145 to Asp-151, Leu-173 to Leu-178.
831178	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1167 as residues: Glu-37 to Asn-42, Ser-48 to Thr-54, Pro-101 to Glu-106.
831184	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1168 as residues: Gln-1 to Pro-29.
831203	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1169 as residues: Thr-1 to Ser-6, Leu-10 to Asn-23, Gln-31 to Arg-36, Arg-43 to His-49, Ala-58 to Leu-63, Gln-81 to Asp-105, Glu-113 to Ile-122, Pro-132 to Lys-137, Ser-175 to Gln-181.
831257	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1173 as residues: Arg-87 to Leu-96, His-104 to Lys-112, Asp-144 to Pro-150.
831277	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1174 as residues: Arg-1 to Gly-13.
831317	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1175 as residues: Ser-97 to Lys-102, Thr-108 to Gly-119, Lys-151 to Gly-157, Pro-204 to Glu-210, Gln-224 to Gly-230, Val-238 to Cys-245, Met-279 to Asn-284, Gly-332 to Glu-349.
831339	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1176 as

	residues: Met-1 to His-19, Pro-21 to Pro-27, Ala-49 to Gly-59, Pro-82 to Ala-104.
831363	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1177 as residues: Thr-1 to Ser-14, Thr-82 to Pro-89, Met-102 to Ala-109, Phe-117 to Ile-124, Asp-142 to Arg-148, Thr-196 to Trp-205, Gln-304 to Leu-310, Gln-325 to Ser-331, Gly-387 to Thr-393, Ala-415 to Lys-430, Pro-469 to Pro-477, Gly-500 to Ile-506, Arg-521 to Gly-529, Pro-534 to Gly-541, Gln-553 to Lys-558, Ala-571 to Glu-579.
831385	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1180 as residues: Ser-1 to Thr-9, Ala-32 to Asn-37, Thr-40 to Tyr-49, Gln-71 to Thr-80.
831390	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1181 as residues: Trp-50 to Gly-55, Leu-109 to Val-119, Phe-146 to Asp-158, Ser-165 to Trp-172, Phe-192 to Ile-197, Leu-241 to Asp-252, Lys-268 to Pro-273, Ser-310 to Lys-315, Asp-334 to Ala-342, Pro-348 to Tyr-353.
831391	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1182 as residues: Ser-28 to Pro-38, Pro-45 to Cys-55, Leu-70 to Ser-77, Glu-98 to Phe-104, Asp-112 to Ser-122, Thr-152 to Lys-158.
831405	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1183 as residues: Asp-47 to Ser-55, Glu-86 to Cys-95, Glu-105 to Gly-113, Gln-133 to Asn-138, Arg-144 to Asp-156.
831476	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1185 as residues: Gln-28 to Gly-33, Asp-41 to Trp-47, Asn-51 to Ser-56, Ser-73 to Asn-83, Trp-111 to Asn-117, Leu-133 to Gln-138, Arg-143 to Tyr-150, Thr-156 to Glu-165.
831488	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1186 as residues: Glu-53 to Asn-59, Lys-97 to Phe-104, Lys-133 to Ala-138.
831519	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1188 as residues: Ser-17 to Gly-25, Thr-47 to Leu-59, His-71 to Arg-77, Pro-83 to Gln-90, Tyr-133 to Ser-143, Arg-160 to Gly-169, Pro-188 to Val-193, Glu-202 to Glu-208, Leu-283 to Arg-288, Glu-295 to Leu-301, Ala-327 to Leu-333, Ala-426 to Pro-433, Leu-444 to Leu-456, Asn-492 to Ala-498.
831550	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1190 as residues: Arg-1 to Gly-15, Ser-42 to Trp-51, Pro-59 to Arg-64.
831560	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1191 as residues: Arg-58 to Asp-64.
831570	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1193 as residues: Thr-61 to Cys-74, Gly-92 to Cys-104, Cys-128 to Ser-133, Asn-179 to Gly-186, Ser-198 to Cys-226, Asn-265 to Ser-274, Ser-280 to Ile-285, Ser-291 to Asp-297, Leu-305 to Gly-315, Phe-317 to Gly-333, Asp-336 to Leu-344, Phe-354 to Cys-361.
831596	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1195 as residues: Gln-80 to Gly-85.
831627	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1196 as residues: Arg-1 to Ser-12, Gly-94 to Thr-106, Ser-161 to Leu-169, Ser-183 to Val-188, Glu-199 to Cys-205, Ser-246 to Ile-251, Leu-271 to Thr-276.
831649	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1197 as residues: Tyr-32 to Lys-39.
831664	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1198 as residues: Lys-1 to Asp-42, Arg-71 to Ala-76, Gln-138 to Phe-145, Lys-170 to Thr-178, Cys-186 to Asp-192.
831684	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1200 as residues: Ile-135 to Ala-140, Tyr-151 to Asn-157, Ser-183 to Ile-190, Gly-196 to Lys-201, Lys-226 to Lys-232, Asn-246 to Thr-252, Asp-293 to Gly-300.
831687	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1201 as residues: Ala-56 to Tyr-63.
831726	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1202 as residues: Arg-3 to Arg-15, Lys-34 to Thr-39, Asn-41 to Lys-59, Ala-104 to Glu-110.
831762	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1204 as residues: Pro-83 to Leu-91, His-116 to Ala-122, Pro-141 to Ser-155.
831848	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1206 as

	residues: Gln-16 to Thr-23.
831861	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1207 as residues: Ala-20 to Lys-26, Pro-59 to Pro-67, Ser-104 to Thr-121, Gln-130 to Gln-136.
831866	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1208 as residues: Arg-11 to Ala-24, Ile-39 to Lys-45, Arg-76 to Pro-85, Lys-124 to Lys-130, Pro-139 to Ser-153, Ala-156 to Glu-170, Ser-179 to Thr-184, Asp-234 to Gly-244, Gly-321 to Lys-329.
831899	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1210 as residues: Asp-11 to Trp-16, Pro-37 to Thr-44, Pro-74 to Pro-82, Arg-112 to Gln-119, Cys-126 to Arg-138, Arg-199 to Thr-204.
831913	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1211 as residues: Pro-22 to Cys-27, Glu-54 to Glu-60, Asp-112 to Phe-117, Lys-183 to Asp-189, Gln-277 to Tyr-282, Pro-325 to Arg-331, Gly-336 to Tyr-346.
831985	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1213 as residues: Cys-7 to Asp-12, Pro-21 to Gly-26.
831986	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1214 as residues: Cys-1 to Ser-7, Ala-62 to Gly-72, Pro-83 to Ala-101.
832010	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1215 as residues: Leu-1 to Lys-21, Glu-39 to Cys-47, Lys-49 to Gln-61, His-64 to Gly-76, Thr-83 to Lys-90, His-92 to Ile-99.
832016	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1216 as residues: Phe-28 to Asn-33, Leu-55 to Tyr-80, Pro-126 to Gly-132, Pro-162 to Gly-169, Pro-194 to Arg-201.
832041	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1217 as residues: Lys-55 to Met-63, Arg-120 to Asp-132, Gly-266 to Glu-281, Val-313 to Thr-319, Leu-361 to Ser-370, Tyr-406 to Met-412, Leu-465 to Trp-470.
832049	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1219 as residues: Leu-80 to Lys-87, Lys-102 to Thr-109, Glu-195 to Thr-200, Thr-203 to Asp-209.
832122	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1220 as residues: Asn-29 to Phe-36, Asp-41 to Ser-50.
832197	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1222 as residues: Glu-61 to Leu-70.
832237	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1223 as residues: Lys-28 to Val-35, Arg-41 to Arg-55, Pro-76 to Thr-87.
832246	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1224 as residues: Arg-17 to Asn-23, Arg-90 to Gly-95, Leu-114 to Glu-121, Pro-153 to Asp-158.
832256	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1225 as residues: Gly-15 to Asn-22.
832280	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1226 as residues: Glu-1 to Trp-16, Ala-32 to Glu-38, Ala-49 to Gln-55, Pro-61 to Gln-66, Ala-78 to Asp-100, Leu-107 to Thr-127, Pro-133 to Phe-157, Pro-160 to Thr-171, Leu-179 to Asp-196, Asp-201 to Lys-222, Pro-249 to Ile-254, Val-258 to Val-263, Thr-268 to Ser-277, Thr-279 to Ala-295, Gly-299 to Phe-327, Val-335 to Asp-346, Lys-366 to Asp-378.
832285	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1227 as residues: Phe-18 to Leu-23.
832294	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1228 as residues: Pro-21 to Gln-28, Pro-56 to Leu-64, Glu-79 to Pro-95, Met-125 to Gly-138.
832326	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1229 as residues: Ser-30 to Trp-45, Gln-64 to Cys-72, Pro-74 to Pro-80, Ala-92 to Arg-98, Trp-104 to Ser-112, Ser-129 to Asp-135, Pro-145 to Gln-152, Arg-168 to Gly-173, Gln-176 to Pro-183.
832370	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1232 as residues: Ala-5 to Ala-11, Pro-23 to Pro-36, Glu-72 to Gly-82, Pro-85 to Pro-91, Asp-

	98 to Gly-119, Pro-121 to Glu-127.
832381	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1233 as residues: Arg-1 to Glu-6, Arg-52 to Ala-58, Phe-72 to Leu-79, Gly-88 to Glu-93, Tyr-124 to Arg-134.
832454	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1235 as residues: Ala-23 to Asp-41.
832465	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1236 as residues: Ala-1 to Gly-7, Ala-32 to Val-45, Ile-65 to Ser-75, Ser-93 to Ser-108.
832475	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1237 as residues: Arg-1 to Val-10, Thr-65 to Ser-71, Arg-83 to Tyr-96, Trp-104 to Trp-111.
832495	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1238 as residues: Arg-9 to Arg-14.
832498	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1239 as residues: Pro-26 to Asp-31, Thr-113 to Gly-125, Asn-158 to Glu-163, Asn-288 to Val-293.
832501	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1240 as residues: Ser-8 to Glu-13.
832505	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1241 as residues: Ala-27 to Arg-46, Pro-54 to Arg-76, Arg-134 to Lys-140, Asn-148 to Ser-154, Lys-166 to Thr-172, Pro-175 to Gln-182, Asp-185 to Asp-192.
832554	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1243 as residues: Arg-26 to Val-31, Asn-122 to Thr-128.
832569	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1244 as residues: Gln-6 to Met-16.
832578	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1245 as residues: Arg-15 to Leu-27, Ser-62 to Gly-72, Pro-107 to His-112, Pro-122 to Gln-142, Glu-147 to Arg-158, Lys-177 to Lys-191, Leu-195 to Val-202, Leu-206 to Pro-218, Glu-228 to Gln-233, Asp-239 to Asp-244, Glu-258 to Gln-278.
832615	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1246 as residues: Gln-41 to Ala-48.
832632	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1248 as residues: Asn-60 to Val-70, Glu-93 to Trp-107, Arg-116 to Gln-125, Leu-133 to Lys-141, Lys-162 to Glu-167.
832633	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1249 as residues: Gly-8 to Trp-13, Pro-36 to Gly-41, Pro-91 to Ala-96.
834859	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1252 as residues: Tyr-16 to Leu-22, Asp-24 to Asp-34, Gly-43 to Ala-48, Gly-57 to Thr-68, Gly-118 to Ser-127, Ile-129 to Tyr-134, Pro-139 to Asp-162.
834861	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1253 as residues: Glu-14 to Glu-50, Glu-67 to Asp-74, Leu-89 to Asn-95.
834890	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1254 as residues: Arg-8 to Lys-13, Gly-35 to Lys-42, Ala-48 to Lys-54, Ala-105 to Leu-110, Gly-150 to Val-157, Phe-164 to Asn-173.
835079	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1255 as residues: Ser-53 to Pro-60.
835554	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1256 as residues: Ile-31 to Ile-38, Asp-116 to Arg-121, Phe-246 to Leu-251, Lys-280 to Tyr-291, Met-363 to Arg-373, Gly-381 to Trp-386.
835723	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1258 as residues: Glu-20 to Thr-26, Trp-47 to Ser-57, Pro-98 to Asn-105, Pro-124 to Phe-129, Ala-173 to Val-183, Lys-190 to Ser-196, Asn-277 to Asn-284, Glu-297 to Phe-306, Thr-322 to Lys-327, Gln-372 to Val-383, Pro-387 to Gly-395, Ser-406 to Thr-415, Arg-432 to Thr-442.
835791	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1259 as residues: Ala-4 to Gly-10.
835817	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1260 as

	residues: Glu-37 to Leu-43.
835840	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1261 as residues: Gln-1 to Asn-6, Pro-18 to Ile-31.
836048	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1262 as residues: Lys-1 to Lys-11, Tyr-27 to Glu-35, Glu-61 to Gly-68.
836898	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1263 as residues: Gln-94 to Lys-102, Gly-140 to Thr-154, Arg-173 to Asp-196, Thr-201 to Asp-206, Glu-241 to Gly-248.
836927	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1264 as residues: His-1 to Arg-12.
837344	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1265 as residues: Pro-15 to Ile-24.
837789	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1266 as residues: Ser-1 to Trp-7, Asp-47 to Ile-52, Pro-70 to Ser-80, Cys-89 to Thr-98, Ala-131 to Ser-142, Phe-169 to Cys-176, Gly-183 to Ser-193, Phe-202 to Pro-209, Arg-243 to Ala-249, Ser-256 to Lys-265, Arg-277 to Asp-284.
838754	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1268 as residues: Phe-27 to Ser-37, Tyr-91 to Arg-96, Pro-156 to Gln-164, Cys-207 to Val-216, Met-242 to Tyr-251.
839561	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1271 as residues: Arg-2 to Gly-7, Arg-16 to Gln-22, Phe-41 to Gly-49, Ala-60 to Asn-74, Leu-125 to Gln-131, Asp-170 to Pro-175, Ala-209 to Arg-218, Glu-222 to Glu-258, Ala-265 to Ser-300.
839816	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1272 as residues: His-32 to Arg-37, Ser-42 to Ser-48, Glu-77 to Glu-88.
840068	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1273 as residues: Ala-1 to Gln-14.
840279	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1274 as residues: Ala-1 to Asp-15.
840538	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1276 as residues: Ala-8 to Pro-13, Pro-18 to Gln-26, Lys-107 to Pro-114, Ala-149 to Arg-157, Ile-294 to Leu-299, Ser-356 to Pro-363, Pro-384 to Phe-392, Ala-474 to Gly-481, Ala-489 to Tyr-494, Pro-512 to Lys-517, Arg-623 to Thr-630, Lys-673 to Ser-678, Thr-703 to His-709, Arg-714 to Arg-720, Gly-755 to Glu-766.
840549	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1278 as residues: Ala-5 to Lys-15, Pro-28 to Gln-34, Tyr-105 to His-111, Gln-150 to Cys-157.
840557	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1280 as residues: Gly-34 to Leu-40, Thr-125 to Gly-134, Ala-148 to Arg-156, Lys-196 to Lys-215.
840561	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1281 as residues: Ser-21 to Phe-30.
840562	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1282 as residues: Gln-33 to Arg-41, Tyr-66 to Glu-71, Thr-112 to Gly-118, Thr-141 to Gly-148, Thr-160 to Cys-168, Arg-171 to Gly-177, Thr-180 to Pro-191, Glu-217 to Asp-225, Asp-236 to Lys-243.
840564	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1283 as residues: Val-13 to Pro-19, Gln-34 to Gly-39.
840600	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1285 as residues: Leu-26 to Ile-39.
840620	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1288 as residues: Ser-17 to Ser-26, His-32 to Gly-42, Thr-78 to Gln-83, Asp-130 to Leu-136, Arg-158 to Pro-164.
840626	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1290 as residues: Phe-7 to Tyr-13, Pro-19 to Ala-35, Asp-87 to Leu-96, Lys-98 to Glu-105, Glu-120 to Leu-133.
840638	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1291 as

	residues: Gly-8 to Leu-13, Gly-21 to Ser-31, Arg-45 to Arg-54.
840649	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1292 as residues: Asn-30 to Thr-37, Asp-44 to Lys-52, Ser-71 to Asp-80, Glu-127 to Glu-133, Arg-162 to Ala-173, Glu-191 to Leu-199.
840651	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1293 as residues: Gly-14 to Glu-38, Asn-90 to Lys-100, Lys-150 to Val-158, Ser-166 to Gly-175.
840681	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1295 as residues: Thr-25 to Gly-31, Pro-86 to Trp-97, Ser-132 to Phe-138.
840682	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1296 as residues: Arg-12 to Lys-19, Asn-30 to Gly-36, Asp-50 to Gly-57, Glu-64 to Thr-69, Thr-79 to Lys-91, Gln-110 to Thr-115, Arg-223 to Gln-229, Asp-255 to Asp-260, Arg-278 to Gly-287, Glu-294 to Gln-300, Glu-433 to Glu-451, Leu-474 to Glu-479, Asp-490 to Leu-498, Gln-519 to Asp-527, Tyr-566 to Asp-575.
840684	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1297 as residues: Pro-1 to Ala-9, Val-56 to Val-63, Gly-86 to Glu-91.
840697	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1298 as residues: Pro-9 to Arg-15, Pro-36 to Ser-42, Ser-65 to Phe-72, Gly-99 to Ser-105, Ala-122 to Phe-129.
840698	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1299 as residues: Thr-75 to Pro-84, His-94 to Met-99, Asp-149 to Ile-168, Asn-370 to Asn-375, Ser-384 to Lys-392, His-427 to Tyr-438.
840708	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1300 as residues: Ala-27 to Ser-36.
840714	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1301 as residues: Gly-1 to Gly-20, Arg-54 to His-59, Asn-89 to Leu-95, Ser-119 to Lys-125, Trp-127 to Cys-133, Gln-175 to Gln-185, Asp-213 to Lys-222, Pro-267 to Gln-275, Asp-306 to Asp-313, Thr-321 to Cys-331.
840716	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1302 as residues: Asn-40 to Thr-45, His-210 to Pro-215, Glu-369 to Thr-375, Lys-383 to Leu-397, Pro-438 to Ile-447, Pro-510 to Tyr-520, Arg-528 to Arg-533, Thr-549 to Thr-555.
840721	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1303 as residues: Arg-1 to Arg-7, Pro-29 to Lys-56, Asp-103 to Arg-108, Tyr-122 to Ser-127, Gly-219 to Glu-227, Asp-250 to Glu-255, Glu-294 to Pro-301, Ala-321 to Tyr-327, Arg-367 to Pro-373, Glu-396 to Asn-405, Gly-411 to Arg-418, Asn-433 to Lys-441.
840735	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1304 as residues: Glu-1 to Gly-11, Thr-20 to Asp-40, Gly-51 to Glu-61, Ala-64 to Leu-78, Leu-82 to Arg-94.
840738	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1305 as residues: Gln-26 to Asn-34.
840745	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1306 as residues: Gln-7 to Gly-12, Leu-60 to Pro-65, Arg-85 to Lys-99, Ser-132 to Pro-145, Pro-150 to Asp-155, Pro-183 to Asn-193, Arg-200 to Tyr-206.
840747	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1307 as residues: Gln-1 to Asp-15, Ile-35 to Glu-41, Leu-66 to Asn-71, Leu-73 to Pro-79, Gln-87 to Lys-94, Val-117 to Arg-123, Pro-144 to Tyr-150.
840756	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1308 as residues: Arg-8 to Gln-19, Arg-25 to Lys-38.
840776	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1309 as residues: Val-2 to Pro-10, Ser-28 to Ala-33, Pro-39 to Tyr-44, Thr-46 to Trp-55, Ser-64 to Ser-72, Ala-103 to Pro-109, Pro-111 to Gln-118.
840784	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1310 as residues: Pro-9 to Gly-20, Asn-32 to Leu-42, Asn-60 to Lys-70, Pro-76 to Gln-81, Glu-86 to Val-93, Arg-106 to Arg-111, Lys-176 to Asn-183.
840788	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1311 as residues: Ser-1 to Gln-8, Val-40 to Ser-49, Arg-105 to Lys-110.

840794	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1312 as residues: Arg-1 to Gln-14, Arg-43 to Glu-54.
840797	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1313 as residues: Gly-1 to Arg-9, Asn-31 to Asp-37, Arg-44 to Asn-53, Gly-62 to Lys-77, Thr-123 to Ile-137, Gly-389 to Thr-394, Lys-486 to Asn-493, Glu-512 to Phe-520, Met-555 to Lys-560, Leu-618 to Ser-623, Ile-698 to Glu-706, Gly-723 to Leu-730, Ala-773 to Gln-790.
840818	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1315 as residues: Pro-1 to Ile-12, Asp-30 to Tyr-35, Leu-38 to Pro-45, Lys-54 to Thr-60, Thr-75 to Leu-80, Asp-92 to Tyr-100, Ile-133 to Thr-138, Thr-194 to Glu-199, Asp-233 to Leu-239, Met-243 to Ala-251, Asp-254 to Glu-261.
840822	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1316 as residues: Val-100 to Tyr-106, Ala-127 to His-135, Gln-153 to Lys-158, Gly-214 to Glu-219, Gln-236 to His-244, Lys-253 to Tyr-258.
840846	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1318 as residues: Ala-20 to Thr-27, Glu-47 to Tyr-57, Tyr-87 to Lys-95, Pro-121 to Ala-127, Pro-208 to Ala-224.
840848	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1319 as residues: Arg-77 to Asn-82, Glu-119 to Arg-124, Gln-156 to Thr-162, Lys-209 to Lys-215.
840860	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1320 as residues: Ile-27 to Asp-41, Glu-43 to Ala-58, Glu-149 to Glu-154, Lys-158 to Ile-165, Glu-167 to Gly-189, Glu-242 to Phe-247, Arg-259 to Phe-268, Ile-283 to Val-291, Thr-295 to Thr-307, Glu-328 to Asp-338, Asp-372 to Gly-387.
840871	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1322 as residues: Gly-31 to Tyr-38, Leu-40 to Leu-45, Pro-203 to Trp-208.
840874	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1323 as residues: Ala-23 to Gly-28.
840878	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1324 as residues: Thr-40 to Glu-46, Pro-69 to Arg-76, Glu-108 to Asp-150.
840880	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1325 as residues: Ser-5 to Lys-14, Phe-32 to Gln-37.
840884	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1326 as residues: Leu-4 to Ser-10.
840926	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1328 as residues: Met-6 to Thr-15, Ser-17 to Phe-37, Ser-148 to Lys-154, Lys-260 to Phe-276, Glu-285 to Ile-292, Lys-410 to Asp-424.
840932	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1329 as residues: Tyr-75 to Pro-83, Ile-181 to Gln-191, Glu-267 to Leu-275, Met-301 to Ala-307, Phe-322 to Gln-328, Met-371 to Gly-381, Gln-458 to Leu-463, Glu-474 to Lys-480, Lys-551 to Ser-558.
840940	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1330 as residues: Ser-26 to Thr-34, Thr-80 to Lys-88.
840947	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1331 as residues: Ile-1 to Arg-11, Pro-19 to Gln-46, Ala-55 to Pro-62, Cys-65 to Cys-82, Lys-93 to Pro-108.
840964	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1333 as residues: Ser-41 to Cys-46.
840979	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1334 as residues: Tyr-10 to His-27, Tyr-31 to Arg-41, Thr-44 to Leu-61, Cys-68 to Phe-73, Lys-98 to Glu-106, Gln-132 to Val-142, Glu-184 to Leu-191.
840984	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1335 as residues: Arg-38 to Gln-48, Met-137 to Asn-144, Gln-167 to Gln-172, Lys-182 to Gln-189, Gln-196 to Glu-206, Ile-210 to Glu-223, Gln-225 to Arg-246, Glu-250 to Thr-269, Gln-296 to Ile-318, Arg-323 to Glu-328, Tyr-337 to Lys-343, Glu-349 to Thr-357, Ser-393 to Glu-403, Arg-405 to Ile-427, Arg-431 to Glu-442, Leu-446 to Lys-473, Glu-475

	to Leu-486, Ile-488 to Asp-503, Ser-505 to Arg-623, Ala-625 to Asn-631, His-634 to Trp-792, Gly-799 to Gly-870, Arg-872 to Glu-929, Ser-931 to Pro-954, Ala-957 to Ala-977, Glu-982 to Trp-1000.
840986	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1336 as residues: Asp-41 to Tyr-51.
840988	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1337 as residues: Pro-17 to Leu-31, Ser-95 to Val-100, Lys-123 to Gly-129.
840990	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1338 as residues: Met-9 to Glu-16, Glu-41 to Trp-47, Arg-55 to Glu-62, Asp-135 to Ile-146, Gly-154 to Gly-160, Met-207 to Phe-214, Ser-245 to Lys-252, Gln-282 to Gln-288.
841009	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1340 as residues: Glu-12 to Thr-27, Met-45 to Asn-52, Tyr-79 to Thr-87, Asp-97 to Gly-102, Met-112 to Asp-120, Pro-141 to Tyr-155.
841012	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1341 as residues: Lys-36 to Ile-44, Arg-49 to Lys-69.
841016	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1342 as residues: Cys-75 to His-82, Asp-126 to Tyr-135, Pro-144 to Tyr-155, Gly-179 to Trp-198, Tyr-201 to Met-208, Pro-226 to Lys-234, Gln-249 to Asp-267.
841017	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1343 as residues: Gln-1 to Trp-19.
841021	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1344 as residues: Glu-58 to Gly-63, Leu-75 to Leu-82.
841032	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1345 as residues: Pro-1 to Gly-13, Pro-30 to Ser-57, Gln-61 to Thr-77, Arg-82 to Thr-88, Pro-100 to Lys-105, Gly-119 to Gly-126.
841051	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1346 as residues: Asn-1 to Lys-6, Thr-16 to Glu-21, Asn-45 to Ser-58, Asp-68 to Ser-75.
841064	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1347 as residues: Asp-53 to Pro-58, Glu-78 to Lys-85, Pro-95 to Arg-102, Ser-142 to Arg-148, Lys-209 to Arg-214, Lys-241 to Gly-246, Ser-287 to Leu-292, Lys-307 to Val-313, Arg-389 to Gln-394.
841069	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1348 as residues: Thr-1 to Trp-14, Lys-27 to Leu-44, Glu-59 to Arg-73, Lys-87 to Phe-95, Pro-160 to Asn-166, Leu-212 to Ile-220, Arg-236 to Asp-243.
841072	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1349 as residues: Pro-7 to Arg-12, Phe-71 to Gln-76, Arg-82 to Asp-98, Ala-108 to Glu-128.
841078	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1350 as residues: Arg-32 to Ala-39.
841080	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1351 as residues: Glu-1 to Gly-7, Glu-25 to Gly-33, Ala-54 to Phe-60, Gly-64 to Gln-108, Glu-116 to Ser-122, Pro-130 to Asn-138, Gln-141 to Lys-153, Arg-164 to Ser-172, Leu-186 to Met-194, Pro-197 to Tyr-205, Asp-218 to Lys-229, Thr-236 to Ser-246, Ala-259 to Trp-266, Pro-281 to Pro-287, Cys-291 to Gln-298.
841092	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1353 as residues: Glu-45 to Lys-50.
841095	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1354 as residues: Lys-1 to Ser-19, Gly-33 to Gly-63, Gly-77 to Pro-89, Ser-164 to Ser-180, Ser-233 to Lys-238, Lys-267 to Leu-286.
841096	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1355 as residues: Gly-5 to Leu-12, Tyr-18 to Asp-25, Ile-88 to Ala-125, Ser-129 to Tyr-141, Gln-191 to Gln-196, Thr-290 to Asn-296, Thr-301 to Thr-309, Leu-360 to Ala-365, Leu-367 to Gly-378, Pro-398 to Gly-418, Pro-443 to Gly-454.
841102	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1356 as residues: Ser-61 to Leu-71.
841108	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1358 as residues: Ala-8 to Leu-20, Lys-27 to Arg-33, Arg-40 to Ala-50, Asp-77 to Glu-84,

	Asn-99 to Gly-109.
841119	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1360 as residues: Lys-6 to Ala-14, Ile-68 to Asn-73, Val-84 to Leu-90, Glu-110 to Val-116, Leu-182 to Gly-190, Tyr-264 to Phe-270, Ile-300 to Lys-306, Pro-354 to Glu-367.
841124	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1361 as residues: Ser-21 to Thr-26.
841143	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1363 as residues: Thr-1 to Lys-9, Pro-20 to Gly-27, Gly-29 to Gly-52, Arg-54 to Gly-61, Gly-69 to Gly-75, Ser-79 to Gly-96, Val-130 to Arg-135, His-207 to Asp-212, Val-296 to Leu-310, Arg-327 to Asn-334.
841148	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1364 as residues: Pro-1 to Met-43, Pro-55 to Ala-66, Pro-118 to Glu-128, Arg-181 to Lys-192, Tyr-197 to Thr-207, Trp-278 to Cys-284, Arg-334 to Asp-349.
841155	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1367 as residues: Gly-9 to Arg-24, Glu-69 to Met-74, Leu-86 to Leu-92, Asp-95 to Arg-115.
841163	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1370 as residues: Gly-29 to Gly-35, Ala-37 to Ala-48, Arg-97 to Thr-102, Arg-114 to Leu-119, Lys-144 to Lys-155.
841169	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1371 as residues: Ala-31 to Thr-69, Pro-90 to Pro-95, Pro-117 to Trp-126, Pro-128 to Arg-136.
841172	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1372 as residues: Gly-17 to Arg-35, His-76 to Pro-90, Pro-92 to Cys-103.
841174	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1373 as residues: Arg-1 to Arg-8, Arg-14 to Phe-19.
841179	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1374 as residues: Leu-4 to Met-10, Leu-17 to Tyr-36, Arg-38 to Asp-63, Tyr-82 to Glu-90, Pro-97 to Gly-134, Arg-137 to Pro-148, Thr-160 to Lys-171, Tyr-183 to Asn-228, Gln-249 to Asn-258, Arg-263 to Glu-271, Arg-277 to Gln-296, Phe-298 to Asp-320, Glu-322 to Lys-329, Thr-337 to Thr-343, Glu-356 to Arg-363, Gly-371 to Asp-384.
841183	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1375 as residues: His-1 to Ser-27, Arg-60 to Arg-73, Arg-96 to Asp-124, Asp-131 to Gly-143, Lys-145 to Glu-150.
841186	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1376 as residues: Leu-7 to Val-18, Ser-27 to Pro-57, Arg-124 to Thr-135, Pro-212 to Ser-230, Gly-282 to Lys-287, Lys-441 to Lys-448.
841204	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1377 as residues: Lys-29 to Arg-35, Glu-81 to Arg-87, Ala-251 to Glu-261, Thr-266 to Gly-271, Thr-289 to Glu-295, Gly-328 to Tyr-334, Phe-432 to Lys-438, Asn-440 to Trp-458.
841206	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1378 as residues: Val-17 to Pro-25, Thr-55 to Asp-70, Lys-75 to Leu-81.
841207	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1379 as residues: Pro-9 to Glu-15, Arg-22 to Trp-32, Ser-54 to Glu-62, Asn-92 to Gly-103.
841211	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1380 as residues: Arg-7 to Gly-12, Met-42 to Ser-58, Gln-65 to Asn-73, Glu-91 to Ala-99, Pro-103 to Tyr-109, Arg-174 to Ala-179, His-189 to Gln-196, Asn-208 to Pro-219.
841225	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1381 as residues: Ala-32 to Ala-40, Glu-93 to Phe-103, Lys-173 to Thr-189.
841237	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1383 as residues: Arg-2 to Gln-12, Lys-76 to Ala-86, Tyr-155 to Lys-163, Glu-228 to Leu-234, Lys-263 to Lys-273, Ile-286 to Lys-296.
841241	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1384 as residues: Asp-41 to Ile-52, Thr-59 to Lys-64, Glu-75 to Asn-89, Thr-99 to Thr-105.
841259	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1385 as residues: His-1 to Cys-22, Pro-24 to Pro-30, Tyr-84 to Ser-90, Ser-108 to Glu-118, Val-126 to Arg-143, Asp-175 to Gln-181, Ser-217 to Gly-224, Cys-262 to Cys-270,

	Tyr-296 to Glu-302, Thr-317 to Thr-324, Gln-341 to Gln-348, Trp-394 to Pro-399.
841260	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1386 as residues: Ala-25 to Glu-32, Ala-48 to Phe-53, Ser-69 to Ser-76, Asp-80 to Glu-86, Ser-125 to Ser-132, Ser-168 to Glu-179, Asn-201 to Ala-206, Lys-216 to Ile-246, Met-259 to Asn-272, Tyr-277 to Gln-287.
841264	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1387 as residues: Met-34 to Gly-50, Asp-69 to Trp-90, Asp-99 to Lys-107, Val-164 to Thr-170.
841311	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1389 as residues: Arg-4 to Val-15.
841313	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1390 as residues: His-6 to Gly-16, Gly-60 to Pro-95, Pro-125 to Gly-131, Gly-138 to Ala-147, Gln-173 to Glu-178.
841322	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1392 as residues: Lys-6 to Arg-23, Ser-74 to Arg-86, Lys-116 to Lys-122, Ser-127 to His-133, Ser-269 to Pro-275, Glu-344 to Phe-350, Gly-356 to His-362.
841331	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1393 as residues: Ser-45 to Lys-67, Asp-155 to Asp-172, Gln-193 to Ile-199, Gln-271 to Glu-285.
841332	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1394 as residues: Glu-8 to Ser-13, Lys-20 to Glu-27, Arg-81 to Ser-94, Thr-147 to Ile-154, Asn-200 to Glu-212, Asn-235 to Gly-244, Leu-433 to Thr-439, Pro-444 to Asn-455, Ser-470 to Asp-476, Ser-492 to Met-499, Glu-535 to Pro-547, Glu-703 to Thr-709, Glu-719 to Thr-726, Asn-802 to Leu-807, Asn-820 to Arg-825, Lys-830 to Tyr-836, Thr-838 to Thr-850, Ser-882 to Ser-894, Lys-944 to Gly-952, Gly-969 to Val-977, Glu-984 to Asn-990, Arg-996 to Lys-1001, Pro-1032 to Leu-1039, Thr-1050 to Gly-1058, Val-1103 to Arg-1108, Pro-1160 to His-1169, Tyr-1180 to Ser-1187, Glu-1211 to Ser-1217, Pro-1277 to Leu-1282.
841338	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1395 as residues: Ser-13 to Ser-18, Phe-48 to Ser-54.
841345	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1396 as residues: Trp-83 to Thr-89, Ser-135 to Asn-140, Ser-185 to Cys-190, Tyr-209 to Glu-220, Val-224 to Glu-232, Leu-258 to Asn-263, Ser-306 to Asn-312, Thr-319 to Glu-327, Thr-365 to Ile-373, Gly-417 to Cys-429, Lys-439 to Val-445, Lys-464 to Leu-469, Leu-477 to Asn-485, Arg-546 to Val-554, Glu-598 to Gly-607, Pro-634 to Ser-639, Asn-730 to Ala-746, Lys-812 to Gln-817, Glu-819 to Lys-835, Leu-867 to Asn-875, Leu-902 to Arg-910.
841349	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1397 as residues: Asp-13 to Arg-18, Pro-36 to Arg-43, Gly-66 to Ser-74, Gly-87 to Lys-92, Asp-110 to Glu-115.
841417	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1399 as residues: Leu-102 to Ile-111, Pro-131 to Ile-337, Thr-339 to Asp-376.
841632	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1401 as residues: Arg-13 to Gly-40, Arg-46 to Glu-52, Gln-55 to Lys-69.
841771	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1403 as residues: Pro-22 to Gly-30, Asp-45 to Gln-56, Ser-67 to Ser-73.
841827	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1404 as residues: Thr-1 to Ser-20.
841835	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1405 as residues: Tyr-5 to Lys-13, Cys-52 to Arg-61, Cys-85 to Ala-91, Gly-122 to Asn-127.
842259	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1406 as residues: Pro-16 to Gly-23, Glu-37 to Pro-45, Gly-52 to Ser-57.
842463	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1407 as residues: Cys-74 to Tyr-79.
842595	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1408 as residues: Pro-93 to Ala-105, Ser-133 to Ser-142, Arg-150 to Glu-155, Lys-220 to Trp-

	226, Glu-257 to Lys-271, Gln-280 to Leu-289.
842722	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1409 as residues: Glu-9 to Arg-20, Ser-48 to Lys-56, Ile-69 to Glu-81, Pro-83 to Lys-89, Lys-94 to Ile-99, Pro-104 to Gly-110, Glu-116 to Asp-133, Ile-140 to Ser-154, Gln-206 to His-217, Pro-219 to Leu-231, Arg-237 to Lys-243, Gln-247 to Pro-256, Leu-271 to Thr-283, Lys-289 to Lys-294, Ser-338 to Lys-355, Gly-375 to Thr-381, Ser-428 to Pro-454, Gly-460 to Gln-467, Lys-480 to Lys-488.
842818	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1411 as residues: Ala-25 to Ala-30, Lys-32 to Ala-51, Gln-61 to Ala-68, Glu-83 to Lys-91, Phe-99 to Glu-105, Glu-123 to Gly-129.
843251	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1412 as residues: Pro-30 to Ser-40, Lys-47 to Thr-52, Val-59 to Pro-64, Lys-129 to Arg-134, Leu-169 to Asp-177.
843422	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1413 as residues: Thr-9 to Lys-20, Lys-25 to Cys-31, Pro-33 to Tyr-42, Asn-76 to Lys-84, Leu-102 to Trp-112.
843784	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1414 as residues: Leu-16 to Thr-24, Glu-41 to Gln-47, Lys-64 to Cys-72, Thr-87 to Ser-100, Pro-130 to Asn-143, Thr-163 to Asp-170.
844017	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1415 as residues: Leu-11 to Ile-17, Leu-30 to Met-45.
844138	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1416 as residues: Lys-19 to Thr-28, Arg-47 to Gln-52, Leu-73 to Leu-81, Asp-122 to Phe-131, Ala-135 to Ser-148, Pro-155 to Asp-163, Ser-184 to His-191, Leu-219 to Asn-225, Asp-238 to Thr-248, Pro-253 to Cys-259, Cys-356 to His-368, Ser-426 to Gly-435, Pro-467 to Cys-478, Glu-504 to Cys-509, His-553 to Gly-568, Ala-581 to Cys-586, Ala-595 to Cys-600, Arg-602 to Trp-608.
844194	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1418 as residues: Pro-23 to Arg-31, Gln-79 to Gln-85, Cys-93 to Cys-107, Pro-216 to Leu-222.
844394	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1419 as residues: Arg-1 to Phe-11.
844450	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1420 as residues: Ser-37 to Trp-43, Pro-47 to Thr-55, Arg-60 to Lys-69, Tyr-125 to His-131, Pro-187 to Lys-195, Gly-346 to Lys-351.
844535	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1422 as residues: Asp-8 to Ala-18, Ser-47 to Ala-52, Thr-62 to Arg-69, Pro-119 to Asp-126, Trp-164 to Thr-170, Ala-206 to Ala-213, Pro-230 to Gly-235, Lys-304 to Lys-314, Lys-341 to Val-347, Tyr-387 to Thr-398.
844644	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1423 as residues: Ala-9 to Asp-16, Asn-78 to Tyr-86.
844653	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1424 as residues: Arg-1 to Gly-8, Ala-30 to Gln-36.
844796	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1426 as residues: His-12 to His-22.
844812	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1427 as residues: Gly-281 to Arg-290, Ala-349 to Ser-355, Glu-378 to Asp-388.
844894	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1428 as residues: Pro-2 to Phe-8, Ser-13 to Ala-34, Pro-37 to Phe-43, Lys-63 to Gly-73, Cys-88 to Asp-93, Gly-98 to Trp-103, Cys-273 to Ile-287, Ile-290 to Ser-296.
845361	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1429 as residues: Met-10 to Ile-21, Glu-108 to Lys-122, Lys-272 to Gly-280, Gly-298 to Lys-304, Trp-364 to Lys-369.
845620	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1430 as residues: Thr-62 to Ala-67, Leu-96 to Glu-101, Cys-184 to Trp-190.
845639	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1431 as residues: Arg-41 to Arg-48, Met-72 to Val-79, Gln-81 to Trp-89, Ala-96 to Asp-101,

	Arg-110 to Gly-118, Asn-126 to Arg-135, Ala-144 to Asp-149, Leu-199 to Lys-213, Gln-245 to Glu-256, Arg-261 to Thr-267.
845660	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1432 as residues: Gly-5 to Leu-17, Arg-19 to Arg-29, Pro-36 to Arg-50, Arg-60 to Pro-67, Gln-133 to Leu-150, Gln-168 to Phe-187, Pro-189 to Gln-194, Asp-240 to Gly-251, Thr-308 to Cys-317, Val-325 to Glu-331, Leu-354 to Pro-369, Lys-381 to Cys-388, Arg-410 to Phe-417.
845720	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1433 as residues: Thr-1 to Glu-11, Arg-21 to Pro-27, Pro-44 to His-49, Glu-56 to Leu-69, Ala-74 to Gly-80, Phe-82 to Pro-87.
845897	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1435 as residues: Gly-1 to Ser-9, Gly-31 to Ser-38, Arg-52 to Val-68, Leu-71 to Glu-84.
845922	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1436 as residues: Asn-1 to Pro-6, Pro-29 to Gln-36, Glu-95 to Arg-100, Pro-150 to Met-157, Ser-272 to Tyr-278, Gly-289 to Arg-294, Lys-397 to Ser-403.
846040	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1438 as residues: Cys-6 to Ser-16, Glu-52 to Tyr-58, Asn-144 to Lys-153.
846073	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1439 as residues: Arg-6 to Thr-16, Ile-43 to Gln-48, Leu-131 to Gly-139, Gly-147 to Asp-155, Asp-191 to Asp-198, Gly-204 to Thr-214.
846257	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1440 as residues: Lys-24 to Phe-44, Arg-58 to Gly-64, Ser-69 to Val-75, Lys-83 to Leu-90, Lys-93 to Glu-106.
HTXPN06R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1441 as residues: Gly-1 to His-8.
HWAFU16R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1443 as residues: Ile-29 to Lys-34.
HOEMT44R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1445 as residues: Asp-73 to Lys-79.
HE2OW04R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1446 as residues: Cys-1 to Asn-6, Met-41 to Thr-51, Lys-77 to Thr-82.
HFCFG25R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1447 as residues: Lys-29 to Ile-37, Arg-42 to Lys-47.
HAPQP94R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1448 as residues: Pro-18 to Arg-23, Ala-43 to Ser-48.
H2CBI37R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1449 as residues: Gly-5 to Lys-19, Phe-26 to Trp-31.
HCRNC25R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1451 as residues: Leu-2 to Asn-8.
H2LAY26R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1453 as residues: Pro-20 to His-36.
HAPQA06R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1454 as residues: Tyr-15 to Ala-22, Ser-68 to Gly-74.
HBGOK18R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1456 as residues: Gly-1 to Tyr-6, Asp-40 to Thr-47, Lys-91 to Glu-97.
HTWKF26R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1458 as residues: Gly-31 to Gly-39.
HTAHR89R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1459 as residues: Asp-73 to Gly-78.
HOELC27R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1461 as residues: Asn-19 to Gln-25, Arg-33 to Ala-42, Pro-92 to Lys-99.
HWLVW62R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1463 as residues: Lys-6 to Phe-13, His-25 to Ser-30, Glu-35 to Ala-41, Pro-57 to Gly-62.
HFKHD94R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1465 as residues: Leu-1 to Gly-6, Pro-29 to Gly-42, Lys-52 to Gly-62.
HOFOA89R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1467 as

	residues: Ala-20 to Lys-29, Arg-48 to Ile-56.
HCROL58R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1470 as residues: Lys-1 to Ser-16.
HCHMV24R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1473 as residues: Gly-4 to Lys-10, Gln-36 to Glu-41.
HCHPT49R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1474 as residues: Gly-4 to Lys-10, Gln-36 to Glu-41, Arg-61 to Arg-70.
HCHPF59R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1477 as residues: Arg-10 to Lys-22.
HS2IA81R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1478 as residues: Gly-4 to Lys-10, Gln-36 to Glu-41, Arg-61 to Arg-76.
HCRNC17R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1479 as residues: Gly-4 to Lys-10, Gln-36 to Glu-41, Arg-61 to Arg-76, Lys-107 to Pro-112.
HISDJ39R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1480 as residues: Gly-4 to Lys-10, Gln-36 to Glu-41, Arg-61 to Arg-76.
HASCG71R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1482 as residues: Lys-6 to Ile-13.
HOEMO43R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1483 as residues: Lys-31 to Gln-43.
HSYDG18R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1486 as residues: Pro-1 to Glu-7, Asp-42 to Gly-47, Leu-61 to Glu-69, Lys-97 to Ile-107, Asp-115 to Gly-120.
HACAC47R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1490 as residues: Ala-18 to Asp-26.
HLQFY41R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1491 as residues: Val-11 to Asp-16, Glu-46 to Arg-51, Pro-55 to Lys-61, Lys-82 to Val-87.
HOFMO83R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1492 as residues: Thr-31 to Asp-39, Thr-52 to Gly-60.
HFTDR22R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1493 as residues: Glu-1 to Trp-13.
HOEKC39R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1495 as residues: Tyr-25 to Phe-32.
HOSNR06R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1498 as residues: Thr-1 to Tyr-7.
HCQDL20R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1499 as residues: Ser-12 to His-21.
HFKHD49R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1503 as residues: Ala-42 to Glu-68.
H6EAQ15R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1506 as residues: Ala-1 to Leu-9.
HCFLM34R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1507 as residues: Lys-7 to Thr-13, Asp-24 to Thr-30, Gly-39 to Glu-52, Leu-70 to Ile-78.
HKIXL19R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1510 as residues: Thr-2 to Asn-12, Gly-14 to Arg-24.
HAJRB09R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1512 as residues: Pro-1 to Glu-8, Ala-10 to Gly-26.
HAPNI86R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1513 as residues: Glu-53 to Ser-59, His-121 to Gln-130.
HAPRJ22R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1515 as residues: Gly-49 to Glu-64, Phe-76 to Thr-81.
HADGE45R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1518 as residues: Arg-1 to Gln-26, Phe-59 to Lys-68.
HTXPN11R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1519 as residues: Asp-1 to Lys-8, Asp-35 to Glu-41.
HCDBN37R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1520 as residues: Cys-1 to Leu-15.

HABGF46R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1527 as residues: Arg-11 to Arg-20, Asn-42 to Pro-57, Arg-64 to Ser-81.
HOELC15R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1528 as residues: His-8 to Gly-18, Gln-56 to Arg-61.
H2LAR26R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1529 as residues: Glu-11 to Asn-16, Lys-38 to Glu-43, Ala-62 to Asp-67, Asp-80 to Ser-101.
H2LAV85R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1530 as residues: Pro-14 to Thr-25, Asp-89 to Gln-102, Ile-121 to Thr-131.
HBSDC92R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1531 as residues: Arg-1 to Leu-11.
HUTHN01R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1532 as residues: Pro-34 to Ser-42, Cys-82 to Lys-89.
H2LAW03R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1533 as residues: Arg-120 to Arg-127.
HOEMO60R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1534 as residues: Pro-6 to Arg-11, Phe-18 to Asn-23, Leu-36 to Thr-41.
HOELF72R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1537 as residues: Arg-1 to Pro-14, Gln-47 to Cys-52.
HAPNX59R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1538 as residues: Cys-19 to Ser-25, Asp-28 to Trp-34, Lys-71 to Trp-76, Glu-112 to Lys-120.
HBJJS17R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1539 as residues: His-14 to Glu-26.
H2CBN02R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1542 as residues: Ala-1 to Pro-9, Arg-20 to Val-25.
H2CBV68R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1543 as residues: Pro-41 to Asp-46, Leu-56 to Lys-61, Ala-72 to Thr-83, Lys-100 to Asn-106, Leu-125 to Thr-133.
H6EDK07R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1544 as residues: Glu-32 to Glu-40, Val-45 to Thr-51, Pro-61 to Arg-67.
H2CBN54R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1547 as residues: Cys-36 to Tyr-44, Glu-55 to Asp-61, Arg-79 to Pro-84, Asp-89 to Pro-105, Cys-108 to Ala-118, Lys-126 to Gly-142.
HWHPX50R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1549 as residues: Pro-35 to Tyr-41.
HAPQD84R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1550 as residues: Lys-32 to Glu-39.
HAMGQ78R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1554 as residues: Arg-46 to Arg-60, Glu-69 to Gly-78.
HODEV64R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1555 as residues: Glu-1 to Gly-27, Asn-34 to Phe-48, Gly-63 to Gly-68.
HOEMK78R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1558 as residues: Asp-27 to Gly-34, Ser-41 to Glu-49, Val-55 to Gln-62.
H2CBD13R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1559 as residues: Ile-17 to His-22, Ser-24 to Arg-29.
HCFMU61R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1560 as residues: Ser-10 to Asp-20, Leu-22 to Pro-36, Ser-42 to Lys-57, Gln-102 to Glu-110.
HOSNE94R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1561 as residues: Arg-1 to Glu-6, Asp-74 to Ser-79, Asp-122 to Thr-127.
HHBEF47R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1563 as residues: Arg-25 to His-31, Ala-50 to Ala-55.
HOSNR67R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1566 as residues: Val-56 to Cys-61, Thr-108 to Gln-122, Gln-125 to Lys-131, Glu-140 to Leu-146.
H2LAV92R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1567 as residues: Leu-3 to Ala-10, Pro-12 to Gly-21, Pro-32 to Pro-38, Ala-58 to Lys-64, Lys-67 to Val-75, Asp-92 to Leu-103.

HCLBZ27R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1570 as residues: Asp-12 to Glu-18, Ala-22 to Ile-28, Ala-48 to Gly-60.
H2LAV11R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1571 as residues: Thr-5 to Thr-14, Arg-20 to His-25, Arg-35 to Gly-40, Lys-58 to Arg-66, His-101 to Ser-107, Arg-111 to Lys-125.
HOEMJ56R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1573 as residues: Lys-27 to Tyr-48.
HDPLP40R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1576 as residues: Gly-1 to Cys-24, Cys-27 to Gly-43, Ala-46 to Trp-54, Ala-56 to Arg-68, Phe-83 to Arg-93.
HABAD57R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1578 as residues: Gly-3 to Gln-16, Pro-36 to Ala-41.
H2CBL68R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1581 as residues: Pro-19 to Val-24, Thr-31 to Gln-38, His-103 to Lys-114, Arg-129 to Leu-137, Pro-139 to Ser-146.
HNTNE17R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1582 as residues: Val-8 to Lys-15, Tyr-25 to Asn-35, Lys-48 to Lys-53, Leu-77 to Asn-87, Asp-103 to Glu-108.
HBJLR37R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1583 as residues: Asn-1 to His-11, Pro-82 to Glu-89, Pro-91 to Asp-96, Arg-103 to Met-109.
HOSNG20R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1584 as residues: Thr-50 to Lys-55.
HBGNY11R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1586 as residues: Thr-10 to Trp-15, Leu-24 to Ala-30, Leu-32 to Glu-38, Asn-41 to Ala-59, Arg-81 to Asp-89, Lys-104 to Lys-111.
HOEKC80R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1587 as residues: Pro-49 to Phe-55, Gly-82 to Gly-88.
HFCES53R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1589 as residues: Thr-12 to Leu-18.
HWAFE36R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1592 as residues: Glu-2 to Ile-9, Glu-34 to Lys-42.
HTXPF20R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1594 as residues: Gly-4 to Thr-13.
HCRMD09R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1595 as residues: Thr-2 to Asn-10, Glu-22 to Gln-30, Ser-58 to Gln-80, Gln-88 to Phe-96, Thr-99 to Tyr-104, Lys-110 to Asp-115.
HAJRB47R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1596 as residues: Trp-18 to Ser-26, Asp-91 to Trp-99.
HAHCR61R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1603 as residues: Ser-17 to Cys-25.
HAPQK19R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1609 as residues: Arg-1 to Lys-10, Ser-15 to Tyr-22, Gly-25 to Leu-31.
HBGOK25R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1615 as residues: Thr-38 to Trp-45, Pro-63 to Gln-70, Pro-78 to Gln-85.
HBJKI05R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1619 as residues: Pro-43 to Trp-50.
HBLGD42R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1621 as residues: Pro-17 to Pro-27, Pro-32 to Tyr-38, Ala-44 to Pro-49.
HCHAK80R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1627 as residues: Gln-3 to His-13, Gly-48 to Gly-55.
HCHMW79R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1628 as residues: Ser-16 to His-21, Ala-29 to Thr-35.
HCHOB92R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1629 as residues: Lys-20 to Lys-28, Ser-53 to Leu-60.
HCLBO01R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1630 as residues: Leu-1 to Leu-18.

HCRPC63R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1633 as residues: Glu-1 to Arg-28.
HCUDC51R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1634 as residues: Pro-22 to Gly-32, Trp-67 to Lys-81.
HDPFI40R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1635 as residues: Tyr-1 to Phe-6, Pro-9 to Asn-22, Arg-30 to Ala-38, Pro-47 to Lys-69.
HDPRZ54R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1637 as residues: Gly-1 to Ala-8.
HFAUO64R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1640 as residues: Asn-7 to Lys-29.
HJMAU64R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1645 as residues: Leu-58 to Tyr-69.
HKBAC48R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1647 as residues: Ser-16 to His-46, Arg-49 to Thr-58.
HKBAD57R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1648 as residues: Thr-23 to Ser-30.
HODAY16R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1653 as residues: Pro-15 to Thr-20.
HOEMO27R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1655 as residues: Ala-7 to Ser-12.
HOEMO62R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1656 as residues: Ile-3 to Lys-11.
HOENU53R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1658 as residues: Lys-37 to Asn-44.
HOGAP33R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1659 as residues: Gln-29 to Asp-35, Gln-43 to Thr-49.
HOSNF25R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1661 as residues: Pro-29 to Arg-36.
HPIAC23R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1663 as residues: Thr-62 to Thr-69.
HRAAD31R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1664 as residues: Val-1 to Thr-6, Arg-64 to Arg-69.
HRADJ57R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1666 as residues: Val-11 to Gln-16.
HROAX48R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1667 as residues: Gly-7 to Thr-20.
HTWDH05R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1670 as residues: Ala-5 to Lys-11, Arg-29 to Ser-36.
HUTHF75R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1673 as residues: Lys-40 to Gly-47.
HWAFW07R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1674 as residues: Phe-44 to Arg-49.
HWLLX91R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1676 as residues: Gly-29 to Asp-34.
HMIAI78R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1678 as residues: Lys-24 to Arg-29, Cys-34 to Ala-41.
HBGFJ39R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1679 as residues: Leu-21 to Asp-38.
HAMHH32R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1680 as residues: Ala-1 to Cys-10, Glu-15 to Gln-21.
HOSNE37R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1683 as residues: Lys-17 to Thr-23.
HWAFE41R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1684 as residues: Ser-3 to Lys-8, Trp-92 to Leu-97.

The present invention encompasses polypeptides comprising, or alternatively consisting of, an epitope of the polypeptide sequence shown in SEQ ID NO:Y, or an epitope of the polypeptide sequence encoded by the cDNA in the related cDNA clone contained in a deposited library or encoded by a polynucleotide that hybridizes to the complement of an epitope encoding sequence of SEQ ID NO:X, or an epitope encoding sequence contained in the deposited cDNA clone under stringent hybridization conditions, or alternatively, under lower stringency hybridization conditions, as defined supra. The present invention further encompasses polynucleotide sequences encoding an epitope of a polypeptide sequence of the invention (such as, for example, the sequence disclosed in SEQ ID NO:X), polynucleotide sequences of the complementary strand of a polynucleotide sequence encoding an epitope of the invention, and polynucleotide sequences which hybridize to this complementary strand under stringent hybridization conditions or alternatively, under lower stringency hybridization conditions, as defined supra.

The term "epitopes," as used herein, refers to portions of a polypeptide having antigenic or immunogenic activity in an animal, preferably a mammal, and most preferably in a human. In a preferred embodiment, the present invention encompasses a polypeptide comprising an epitope, as well as the polynucleotide encoding this polypeptide. An "immunogenic epitope," as used herein, is defined as a portion of a protein that elicits an antibody response in an animal, as determined by any method known in the art, for example, by the methods for generating antibodies described infra. (See, for example, Geysen et al., Proc. Natl. Acad. Sci. USA 81:3998- 4002 (1983)). The term "antigenic epitope," as used herein, is defined as a portion of a protein to which an antibody can immunospecifically bind its antigen as determined by any method well known in the art, for example, by the immunoassays described herein. Immunospecific binding excludes non-specific binding but does not necessarily exclude cross- reactivity with other antigens. Antigenic epitopes need not necessarily be immunogenic.

Fragments which function as epitopes may be produced by any conventional means. (See, e.g., Houghten, R. A., Proc. Natl. Acad. Sci. USA 82:5131-5135 (1985) further described in U.S. Patent No. 4,631,211.)

In the present invention, antigenic epitopes preferably contain a sequence of at least 4, at least 5, at least 6, at least 7, more preferably at least 8, at least 9, at least 10, at least 11, at least 12, at least 13, at least 14, at least 15, at least 20, at least 25, at least 30, at least 40, at least 50, and, most preferably, between about 15 to about 30 amino acids. Preferred polypeptides comprising immunogenic or antigenic epitopes are at least 10, 15, 20, 25, 30, 35, 40, 45, 50, 55, 60, 65, 70, 75, 80, 85, 90, 95, or 100 amino acid residues in length. Additional non-exclusive preferred antigenic epitopes include the antigenic epitopes disclosed herein, as well as portions thereof. Antigenic epitopes are useful, for example, to raise antibodies, including monoclonal antibodies, that specifically bind the epitope. Preferred antigenic epitopes include the antigenic epitopes disclosed herein, as well as any combination of two, three, four, five or more of these antigenic epitopes. Antigenic epitopes can be used as the target molecules in immunoassays. (See, for instance, Wilson et al., Cell 37:767-778 (1984); Sutcliffe et al., Science 219:660-666 (1983)).

Similarly, immunogenic epitopes can be used, for example, to induce antibodies according to methods well known in the art. (See, for instance, Sutcliffe et al., supra; Wilson et al., supra; Chow et al., Proc. Natl. Acad. Sci. USA 82:910-914; and Bittle et al., J. Gen. Virol. 66:2347-2354 (1985). Preferred immunogenic epitopes include the immunogenic epitopes disclosed herein, as well as any combination of two, three, four, five or more of these immunogenic epitopes. The polypeptides comprising one or more immunogenic epitopes may be presented for eliciting an antibody response together with a carrier protein, such as an albumin, to an animal system (such as rabbit or mouse), or, if the polypeptide is of sufficient length (at least about 25 amino acids), the polypeptide may be presented without a carrier. However, immunogenic epitopes comprising as few as 8 to 10 amino acids have been shown to be sufficient to raise antibodies capable of binding to, at the very least, linear epitopes in a denatured polypeptide (e.g., in Western blotting).

Epitope-bearing polypeptides of the present invention may be used to induce antibodies according to methods well known in the art including, but not limited to, in vivo immunization, in vitro immunization, and phage display methods. See, e.g., Sutcliffe et al., supra; Wilson et al., supra, and Bittle et al., J. Gen. Virol., 66:2347-2354 (1985). If in vivo immunization is used, animals may be immunized with free peptide; however, anti-peptide antibody titer may be boosted by coupling the peptide to a macromolecular carrier, such as keyhole limpet hemacyanin (KLH) or tetanus toxoid. For instance, peptides containing cysteine residues may be coupled to a carrier using a linker such as maleimidobenzoyl- N-hydroxysuccinimide ester (MBS), while other peptides may be coupled to carriers using a more general linking agent such as glutaraldehyde. Animals such as rabbits, rats and mice are immunized with either free or carrier- coupled peptides, for instance, by intraperitoneal and/or intradermal injection of emulsions containing about 100 μg of peptide or carrier protein and Freund's adjuvant or any other adjuvant known for stimulating an immune response. Several booster injections may be needed, for instance, at intervals of about two weeks, to provide a useful titer of anti-peptide antibody which can be detected, for example, by ELISA assay using free peptide adsorbed to a solid surface. The titer of anti-peptide antibodies in serum from an immunized animal may be increased by selection of anti-peptide antibodies, for instance, by adsorption to the peptide on a solid support and elution of the selected antibodies according to methods well known in the art.

As one of skill in the art will appreciate, and as discussed above, the polypeptides of the present invention , and immunogenic and/or antigenic epitope fragments thereof can be fused to other polypeptide sequences. For example, the polypeptides of the present invention may be fused with the constant domain of immunoglobulins (IgA, IgE, IgG, IgM), or portions thereof (CH1, CH2, CH3, or any combination thereof and portions thereof) resulting in chimeric polypeptides. Such fusion proteins may facilitate purification and may increase half-life in vivo. This has been shown for chimeric proteins consisting of the first two domains of the human CD4-polypeptide and various domains of the constant regions of the heavy or light

chains of mammalian immunoglobulins. See, e.g., EP 394,827; Traunecker et al., Nature, 331:84-86 (1988). Enhanced delivery of an antigen across the epithelial barrier to the immune system has been demonstrated for antigens (e.g., insulin) conjugated to an FcRn binding partner such as IgG or Fc fragments (see, e.g., PCT Publications WO 96/22024 and WO 99/04813). IgG Fusion proteins that have a disulfide-linked dimeric structure due to the IgG portion desulfide bonds have also been found to be more efficient in binding and neutralizing other molecules than monomeric polypeptides or fragments thereof alone. See, e.g., Fountoulakis et al., J. Biochem., 270:3958-3964 (1995).

Similarly, EP-A-O 464 533 (Canadian counterpart 2045869) discloses fusion proteins comprising various portions of constant region of immunoglobulin molecules together with another human protein or part thereof. In many cases, the Fc part in a fusion protein is beneficial in therapy and diagnosis, and thus can result in, for example, improved pharmacokinetic properties. (EP-A 0232 262.) Alternatively, deleting the Fc part after the fusion protein has been expressed, detected, and purified, may be desired. For example, the Fc portion may hinder therapy and diagnosis if the fusion protein is used as an antigen for immunizations. In drug discovery, for example, human proteins, such as hIL-5, have been fused with Fc portions for the purpose of high-throughput screening assays to identify antagonists of hIL-5. (See, D. Bennett et al., J. Molecular Recognition 8:52-58 (1995); K. Johanson et al., J. Biol. Chem. 270:9459-9471 (1995).)

Moreover, the polypeptides of the present invention can be fused to marker sequences, such as a peptide which facilitates purification of the fused polypeptide. In preferred embodiments, the marker amino acid sequence is a hexa-histidine peptide, such as the tag provided in a pQE vector (QIAGEN, Inc., 9259 Eton Avenue, Chatsworth, CA, 91311), among others, many of which are commercially available. As described in Gentz et al., Proc. Natl. Acad. Sci. USA 86:821-824 (1989), for instance, hexa-histidine provides for convenient purification of the fusion protein. Another peptide tag useful for purification, the "HA" tag, corresponds to an epitope

derived from the influenza hemagglutinin protein. (Wilson et al., Cell 37:767 (1984).)

Thus, any of these above fusions can be engineered using the polynucleotides or the polypeptides of the present invention.

Nucleic acids encoding the above epitopes can also be recombined with a gene of interest as an epitope tag (e.g., the hemagglutinin ("HA") tag or flag tag) to aid in detection and purification of the expressed polypeptide. For example, a system described by Janknecht et al. allows for the ready purification of non-denatured fusion proteins expressed in human cell lines (Janknecht et al., Proc. Natl. Acad. Sci. USA 88:8972- 897 (1991)). In this system, the gene of interest is subcloned into a vaccinia recombination plasmid such that the open reading frame of the gene is translationally fused to an amino-terminal tag consisting of six histidine residues. The tag serves as a matrix binding domain for the fusion protein. Extracts from cells infected with the recombinant vaccinia virus are loaded onto Ni2+ nitriloacetic acid-agarose column and histidine-tagged proteins can be selectively eluted with imidazole-containing buffers.

Additional fusion proteins of the invention may be generated through the techniques of gene-shuffling, motif-shuffling, exon-shuffling, and/or codon-shuffling (collectively referred to as "DNA shuffling"). DNA shuffling may be employed to modulate the activities of polypeptides of the invention, such methods can be used to generate polypeptides with altered activity, as well as agonists and antagonists of the polypeptides. See, generally, U.S. Patent Nos. 5,605,793; 5,811,238; 5,830,721; 5,834,252; and 5,837,458, and Patten et al., Curr. Opinion Biotechnol. 8:724-33 (1997); Harayama, Trends Biotechnol. 16(2):76-82 (1998); Hansson, et al., J. Mol. Biol. 287:265-76 (1999); and Lorenzo and Blasco, Biotechniques 24(2):308- 13 (1998) (each of these patents and publications are hereby incorporated by reference in its entirety). In one embodiment, alteration of polynucleotides corresponding to SEQ ID NO:X and the polypeptides encoded by these polynucleotides may be achieved by DNA shuffling. DNA shuffling involves the assembly of two or more DNA segments by homologous or site-specific recombination to generate variation in the

polynucleotide sequence. In another embodiment, polynucleotides of the invention, or the encoded polypeptides, may be altered by being subjected to random mutagenesis by error-prone PCR, random nucleotide insertion or other methods prior to recombination. In another embodiment, one or more components, motifs, sections, parts, domains, fragments, etc., of a polynucleotide encoding a polypeptide of the invention may be recombined with one or more components, motifs, sections, parts, domains, fragments, etc. of one or more heterologous molecules.

As discussed herein, any polypeptide of the present invention can be used to generate fusion proteins. For example, the polypeptide of the present invention, when fused to a second protein, can be used as an antigenic tag. Antibodies raised against the polypeptide of the present invention can be used to indirectly detect the second protein by binding to the polypeptide. Moreover, because secreted proteins target cellular locations based on trafficking signals, polypeptides of the present invention which are shown to be secreted can be used as targeting molecules once fused to other proteins.

Examples of domains that can be fused to polypeptides of the present invention include not only heterologous signal sequences, but also other heterologous functional regions. The fusion does not necessarily need to be direct, but may occur through linker sequences.

In certain preferred embodiments, proteins of the invention comprise fusion proteins wherein the polypeptides are N and/or C- terminal deletion mutants. In preferred embodiments, the application is directed to nucleic acid molecules at least 80%, 85%, 90%, 95%, 96%, 97%, 98% or 99% identical to the nucleic acid sequences encoding polypeptides having the amino acid sequence of the specific N- and C-terminal deletions mutants. Polynucleotides encoding these polypeptides are also encompassed by the invention.

Moreover, fusion proteins may also be engineered to improve characteristics of the polypeptide of the present invention. For instance, a region of additional amino acids, particularly charged amino acids, may be added to the N-terminus of the polypeptide to improve stability and persistence during purification from the host cell

or subsequent handling and storage. Also, peptide moieties may be added to the polypeptide to facilitate purification. Such regions may be removed prior to final preparation of the polypeptide. The addition of peptide moieties to facilitate handling of polypeptides are familiar and routine techniques in the art.

Vectors, Host Cells, and Protein Production

The present invention also relates to vectors containing the polynucleotide of the present invention, host cells, and the production of polypeptides by recombinant techniques. The vector may be, for example, a phage, plasmid, viral, or retroviral vector. Retroviral vectors may be replication competent or replication defective. In the latter case, viral propagation generally will occur only in complementing host cells.

The polynucleotides of the invention may be joined to a vector containing a selectable marker for propagation in a host. Generally, a plasmid vector is introduced in a precipitate, such as a calcium phosphate precipitate, or in a complex with a charged lipid. If the vector is a virus, it may be packaged in vitro using an appropriate packaging cell line and then transduced into host cells.

The polynucleotide insert should be operatively linked to an appropriate promoter, such as the phage lambda PL promoter, the E. coli lac, trp, phoA and tac promoters, the SV40 early and late promoters and promoters of retroviral LTRs, to name a few. Other suitable promoters will be known to the skilled artisan. The expression constructs will further contain sites for transcription initiation, termination, and, in the transcribed region, a ribosome binding site for translation. The coding portion of the transcripts expressed by the constructs will preferably include a translation initiating codon at the beginning and a termination codon (UAA, UGA or UAG) appropriately positioned at the end of the polypeptide to be translated.

As indicated, the expression vectors will preferably include at least one selectable marker. Such markers include dihydrofolate reductase, G418 or neomycin resistance for eukaryotic cell culture and tetracycline, kanamycin or ampicillin resistance genes for culturing in E. coli and other bacteria. Representative examples

of appropriate hosts include, but are not limited to, bacterial cells, such as E. coli, Streptomyces and Salmonella typhimurium cells; fungal cells, such as yeast cells (e.g., Saccharomyces cerevisiae or Pichia pastoris (ATCC Accession No. 201178)); insect cells such as Drosophila S2 and Spodoptera Sf9 cells; animal cells such as CHO, COS, 293, and Bowes melanoma cells; and plant cells. Appropriate culture mediums and conditions for the above-described host cells are known in the art.

Among vectors preferred for use in bacteria include pQE70, pQE60 and pQE-9, available from QIAGEN, Inc.; pBluescript vectors, Phagescript vectors, pNH8A, pNH16a, pNH18A, pNH46A, available from Stratagene Cloning Systems, Inc.; and ptrc99a, pKK223-3, pKK233-3, pDR540, pRIT5 available from Pharmacia Biotech, Inc. Among preferred eukaryotic vectors are pWLNEO, pSV2CAT, pOG44, pXT1 and pSG available from Stratagene; and pSVK3, pBPV, pMSG and pSVL available from Pharmacia. Preferred expression vectors for use in yeast systems include, but are not limited to pYES2, pYD1, pTEF1/Zeo, pYES2/GS, pPICZ, pGAPZ, pGAPZalph, pPIC9, pPIC3.5, pHIL-D2, pHIL-S1, pPIC3.5K, pPIC9K, and PAO815 (all available from Invitrogen, Carlbad, CA). Other suitable vectors will be readily apparent to the skilled artisan.

Introduction of the construct into the host cell can be effected by calcium phosphate transfection, DEAE-dextran mediated transfection, cationic lipid-mediated transfection, electroporation, transduction, infection, or other methods. Such methods are described in many standard laboratory manuals, such as Davis et al., Basic Methods In Molecular Biology (1986). It is specifically contemplated that the polypeptides of the present invention may in fact be expressed by a host cell lacking a recombinant vector.

A polypeptide of this invention can be recovered and purified from recombinant cell cultures by well-known methods including ammonium sulfate or ethanol precipitation, acid extraction, anion or cation exchange chromatography, phosphocellulose chromatography, hydrophobic interaction chromatography, affinity chromatography, hydroxylapatite chromatography and lectin chromatography. Most

preferably, high performance liquid chromatography ("HPLC") is employed for purification.

Polypeptides of the present invention can also be recovered from: products purified from natural sources, including bodily fluids, tissues and cells, whether directly isolated or cultured; products of chemical synthetic procedures; and products produced by recombinant techniques from a prokaryotic or eukaryotic host, including, for example, bacterial, yeast, higher plant, insect, and mammalian cells. Depending upon the host employed in a recombinant production procedure, the polypeptides of the present invention may be glycosylated or may be non-glycosylated. In addition, polypeptides of the invention may also include an initial modified methionine residue, in some cases as a result of host-mediated processes. Thus, it is well known in the art that the N-terminal methionine encoded by the translation initiation codon generally is removed with high efficiency from any protein after translation in all eukaryotic cells. While the N-terminal methionine on most proteins also is efficiently removed in most prokaryotes, for some proteins, this prokaryotic removal process is inefficient, depending on the nature of the amino acid to which the N-terminal methionine is covalently linked.

In one embodiment, the yeast *Pichia pastoris* is used to express polypeptides of the invention in a eukaryotic system. *Pichia pastoris* is a methylotrophic yeast which can metabolize methanol as its sole carbon source. A main step in the methanol metabolization pathway is the oxidation of methanol to formaldehyde using O_2. This reaction is catalyzed by the enzyme alcohol oxidase. In order to metabolize methanol as its sole carbon source, *Pichia pastoris* must generate high levels of alcohol oxidase due, in part, to the relatively low affinity of alcohol oxidase for O_2. Consequently, in a growth medium depending on methanol as a main carbon source, the promoter region of one of the two alcohol oxidase genes (*AOX1*) is highly active. In the presence of methanol, alcohol oxidase produced from the *AOX1* gene comprises up to approximately 30% of the total soluble protein in *Pichia pastoris*. *See*, Ellis, S.B., *et al.*, *Mol. Cell. Biol.* 5:1111-21 (1985); Koutz, P.J, *et al.*, *Yeast*

5:167-77 (1989); Tschopp, J.F., *et al.*, *Nucl. Acids Res.* 15:3859-76 (1987). Thus, a heterologous coding sequence, such as, for example, a polynucleotide of the present invention, under the transcriptional regulation of all or part of the *AOX1* regulatory sequence is expressed at exceptionally high levels in *Pichia* yeast grown in the presence of methanol.

In one example, the plasmid vector pPIC9K is used to express DNA encoding a polypeptide of the invention, as set forth herein, in a *Pichea* yeast system essentially as described in "*Pichia* Protocols: Methods in Molecular Biology," D.R. Higgins and J. Cregg, eds. The Humana Press, Totowa, NJ, 1998. This expression vector allows expression and secretion of a polypeptide of the invention by virtue of the strong *AOX1* promoter linked to the *Pichia pastoris* alkaline phosphatase (PHO) secretory signal peptide (i.e., leader) located upstream of a multiple cloning site.

Many other yeast vectors could be used in place of pPIC9K, such as, pYES2, pYD1, pTEF1/Zeo, pYES2/GS, pPICZ, pGAPZ, pGAPZalpha, pPIC9, pPIC3.5, pHIL-D2, pHIL-S1, pPIC3.5K, and PAO815, as one skilled in the art would readily appreciate, as long as the proposed expression construct provides appropriately located signals for transcription, translation, secretion (if desired), and the like, including an in-frame AUG as required.

In another embodiment, high-level expression of a heterologous coding sequence, such as, for example, a polynucleotide of the present invention, may be achieved by cloning the heterologous polynucleotide of the invention into an expression vector such as, for example, pGAPZ or pGAPZalpha, and growing the yeast culture in the absence of methanol.

In addition to encompassing host cells containing the vector constructs discussed herein, the invention also encompasses primary, secondary, and immortalized host cells of vertebrate origin, particularly mammalian origin, that have been engineered to delete or replace endogenous genetic material (e.g., coding sequence), and/or to include genetic material (e.g., heterologous polynucleotide sequences) that is operably associated with polynucleotides of the invention, and

which activates, alters, and/or amplifies endogenous polynucleotides. For example, techniques known in the art may be used to operably associate heterologous control regions (e.g., promoter and/or enhancer) and endogenous polynucleotide sequences via homologous recombination (see, e.g., U.S. Patent No. 5,641,670, issued June 24, 1997; International Publication No. WO 96/29411, published September 26, 1996; International Publication No. WO 94/12650, published August 4, 1994; Koller et al., Proc. Natl. Acad. Sci. USA 86:8932-8935 (1989); and Zijlstra et al., Nature 342:435-438 (1989), the disclosures of each of which are incorporated by reference in their entireties).

In addition, polypeptides of the invention can be chemically synthesized using techniques known in the art (e.g., see Creighton, 1983, Proteins: Structures and Molecular Principles, W.H. Freeman & Co., N.Y., and Hunkapiller et al., *Nature*, 310:105-111 (1984)). For example, a polypeptide corresponding to a fragment of a polypeptide can be synthesized by use of a peptide synthesizer. Furthermore, if desired, nonclassical amino acids or chemical amino acid analogs can be introduced as a substitution or addition into the polypeptide sequence. Non-classical amino acids include, but are not limited to, to the D-isomers of the common amino acids, 2,4-diaminobutyric acid, a-amino isobutyric acid, 4-aminobutyric acid, Abu, 2-amino butyric acid, g-Abu, e-Ahx, 6-amino hexanoic acid, Aib, 2-amino isobutyric acid, 3-amino propionic acid, ornithine, norleucine, norvaline, hydroxyproline, sarcosine, citrulline, homocitrulline, cysteic acid, t-butylglycine, t-butylalanine, phenylglycine, cyclohexylalanine, b-alanine, fluoro-amino acids, designer amino acids such as b-methyl amino acids, Ca-methyl amino acids, Na-methyl amino acids, and amino acid analogs in general. Furthermore, the amino acid can be D (dextrorotary) or L (levorotary).

Non-naturally occurring variants may be produced using art-known mutagenesis techniques, which include, but are not limited to oligonucleotide mediated mutagenesis, alanine scanning, PCR mutagenesis, site directed mutagenesis (*see, e.g.*, Carter *et al., Nucl. Acids Res. 13*:4331 (1986); and Zoller *et al., Nucl. Acids Res. 10*:6487 (1982)), cassette mutagenesis (*see, e.g.*, Wells *et al., Gene 34*:315

(1985)), restriction selection mutagenesis (*see, e.g.*, Wells *et al.*, *Philos. Trans. R. Soc. London SerA 317*:415 (1986)).

The invention additionally, encompasses polypeptides of the present invention which are differentially modified during or after translation, e.g., by glycosylation, acetylation, phosphorylation, amidation, derivatization by known protecting/blocking groups, proteolytic cleavage, linkage to an antibody molecule or other cellular ligand, etc. Any of numerous chemical modifications may be carried out by known techniques, including but not limited, to specific chemical cleavage by cyanogen bromide, trypsin, chymotrypsin, papain, V8 protease, $NaBH_4$; acetylation, formylation, oxidation, reduction; metabolic synthesis in the presence of tunicamycin; etc.

Additional post-translational modifications encompassed by the invention include, for example, e.g., N-linked or O-linked carbohydrate chains, processing of N-terminal or C-terminal ends), attachment of chemical moieties to the amino acid backbone, chemical modifications of N-linked or O-linked carbohydrate chains, and addition or deletion of an N-terminal methionine residue as a result of procaryotic host cell expression. The polypeptides may also be modified with a detectable label, such as an enzymatic, fluorescent, isotopic or affinity label to allow for detection and isolation of the protein.

Also provided by the invention are chemically modified derivatives of the polypeptides of the invention which may provide additional advantages such as increased solubility, stability and circulating time of the polypeptide, or decreased immunogenicity (see U.S. Patent No. 4,179,337). The chemical moieties for derivitization may be selected from water soluble polymers such as polyethylene glycol, ethylene glycol/propylene glycol copolymers, carboxymethylcellulose, dextran, polyvinyl alcohol and the like. The polypeptides may be modified at random positions within the molecule, or at predetermined positions within the molecule and may include one, two, three or more attached chemical moieties.

The polymer may be of any molecular weight, and may be branched or unbranched. For polyethylene glycol, the preferred molecular weight is between

about 1 kDa and about 100 kDa (the term "about" indicating that in preparations of polyethylene glycol, some molecules will weigh more, some less, than the stated molecular weight) for ease in handling and manufacturing. Other sizes may be used, depending on the desired therapeutic profile (e.g., the duration of sustained release desired, the effects, if any on biological activity, the ease in handling, the degree or lack of antigenicity and other known effects of the polyethylene glycol to a therapeutic protein or analog). For example, the polyethylene glycol may have an average molecular weight of about 200; 500; 1000; 1500; 2000; 2500; 3000; 3500; 4000; 4500; 5000; 5500; 6000; 6500; 7000; 7500; 8000; 8500; 9000; 9500; 10,000; 10,500; 11,000; 11,500; 12,000; 12,500; 13,000; 13,500; 14,000; 14,500; 15,000; 15,500; 16,000; 16,500; 17,000; 17,500; 18,000; 18,500; 19,000; 19,500; 20,000; 25,000; 30,000; 35,000; 40,000; 50,000; 55,000; 60,000; 65,000; 70,000; 75,000; 80,000; 85,000; 90,000; 95,000; or 100,000 kDa.

As noted above, the polyethylene glycol may have a branched structure. Branched polyethylene glycols are described, for example, in U.S. Patent No. 5,643,575; Morpurgo *et al., Appl. Biochem. Biotechnol. 56*:59-72 (1996); Vorobjev *et al., Nucleosides Nucleotides 18*:2745-2750 (1999); and Caliceti *et al., Bioconjug. Chem. 10*:638-646 (1999), the disclosures of each of which are incorporated herein by reference.

The polyethylene glycol molecules (or other chemical moieties) should be attached to the protein with consideration of effects on functional or antigenic domains of the protein. There are a number of attachment methods available to those skilled in the art, e.g., EP 0 401 384, herein incorporated by reference (coupling PEG to G-CSF), see also Malik et al., Exp. Hematol. 20:1028-1035 (1992) (reporting pegylation of GM-CSF using tresyl chloride). For example, polyethylene glycol may be covalently bound through amino acid residues via a reactive group, such as, a free amino or carboxyl group. Reactive groups are those to which an activated polyethylene glycol molecule may be bound. The amino acid residues having a free amino group may include lysine residues and the N-terminal amino acid residues; those having a free carboxyl group may include aspartic acid residues glutamic acid

residues and the C-terminal amino acid residue. Sulfhydryl groups may also be used as a reactive group for attaching the polyethylene glycol molecules. Preferred for therapeutic purposes is attachment at an amino group, such as attachment at the N-terminus or lysine group.

As suggested above, polyethylene glycol may be attached to proteins via linkage to any of a number of amino acid residues. For example, polyethylene glycol can be linked to a proteins via covalent bonds to lysine, histidine, aspartic acid, glutamic acid, or cysteine residues. One or more reaction chemistries may be employed to attach polyethylene glycol to specific amino acid residues (e.g., lysine, histidine, aspartic acid, glutamic acid, or cysteine) of the protein or to more than one type of amino acid residue (e.g., lysine, histidine, aspartic acid, glutamic acid, cysteine and combinations thereof) of the protein.

One may specifically desire proteins chemically modified at the N-terminus. Using polyethylene glycol as an illustration of the present composition, one may select from a variety of polyethylene glycol molecules (by molecular weight, branching, etc.), the proportion of polyethylene glycol molecules to protein (polypeptide) molecules in the reaction mix, the type of pegylation reaction to be performed, and the method of obtaining the selected N-terminally pegylated protein. The method of obtaining the N-terminally pegylated preparation (i.e., separating this moiety from other monopegylated moieties if necessary) may be by purification of the N-terminally pegylated material from a population of pegylated protein molecules. Selective proteins chemically modified at the N-terminus modification may be accomplished by reductive alkylation which exploits differential reactivity of different types of primary amino groups (lysine versus the N-terminal) available for derivatization in a particular protein. Under the appropriate reaction conditions, substantially selective derivatization of the protein at the N-terminus with a carbonyl group containing polymer is achieved.

As indicated above, pegylation of the proteins of the invention may be accomplished by any number of means. For example, polyethylene glycol may be attached to the protein either directly or by an intervening linker. Linkerless systems

for attaching polyethylene glycol to proteins are described in Delgado *et al., Crit. Rev. Thera. Drug Carrier Sys. 9*:249-304 (1992); Francis *et al., Intern. J. of Hematol. 68*:1-18 (1998); U.S. Patent No. 4,002,531; U.S. Patent No. 5,349,052; WO 95/06058; and WO 98/32466, the disclosures of each of which are incorporated herein by reference.

One system for attaching polyethylene glycol directly to amino acid residues of proteins without an intervening linker employs tresylated MPEG, which is produced by the modification of monmethoxy polyethylene glycol (MPEG) using tresylchloride ($ClSO_2CH_2CF_3$). Upon reaction of protein with tresylated MPEG, polyethylene glycol is directly attached to amine groups of the protein. Thus, the invention includes protein-polyethylene glycol conjugates produced by reacting proteins of the invention with a polyethylene glycol molecule having a 2,2,2-trifluoreothane sulphonyl group.

Polyethylene glycol can also be attached to proteins using a number of different intervening linkers. For example, U.S. Patent No. 5,612,460, the entire disclosure of which is incorporated herein by reference, discloses urethane linkers for connecting polyethylene glycol to proteins. Protein-polyethylene glycol conjugates wherein the polyethylene glycol is attached to the protein by a linker can also be produced by reaction of proteins with compounds such as MPEG-succinimidylsuccinate, MPEG activated with 1,1'-carbonyldiimidazole, MPEG-2,4,5-trichloropenylcarbonate, MPEG-p-nitrophenolcarbonate, and various MPEG-succinate derivatives. A number additional polyethylene glycol derivatives and reaction chemistries for attaching polyethylene glycol to proteins are described in WO 98/32466, the entire disclosure of which is incorporated herein by reference. Pegylated protein products produced using the reaction chemistries set out herein are included within the scope of the invention.

The number of polyethylene glycol moieties attached to each protein of the invention (*i.e.*, the degree of substitution) may also vary. For example, the pegylated proteins of the invention may be linked, on average, to 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 12, 15, 17, 20, or more polyethylene glycol molecules. Similarly, the average degree of